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OM nucleic - nucleic search, using SW model

Run on: October 8, 2005, 02:13:36 ; Search time 964 Seconds
(without alignments)
8496.529 Million cell updates/sec

Title: US-10-626-445-5

Perfect score: 1176

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Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16886260

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1176	100.0	1176	20	US-10-626-445-5
2	1176	100.0	1176	21	US-10-626-126-5
3	1176	100.0	1176	21	US-10-626-138-5
4	958.4	81.5	1176	20	US-10-626-445-6
5	958.4	81.5	1176	21	US-10-626-126-6
6	958.4	81.5	1176	21	US-10-626-138-6
7	686.6	58.4	1173	9	US-09-812-216-1

8	686.6	58.4	1173	9	US-09-910-411-1	Sequence 1, Appl1
9	686.6	58.4	1173	10	US-09-875-076-13	Sequence 13, Appl1
10	686.6	58.4	1173	10	US-09-876-252-13	Sequence 13, Appl1
11	686.6	58.4	1173	13	US-10-052-193-1	Sequence 1, Appl1
12	686.6	58.4	1173	15	US-10-272-983-13	Sequence 13, Appl1
13	686.6	58.4	1173	15	US-10-354-769-1	Sequence 1, Appl1
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15	686.6	58.4	1173	17	US-10-417-820A-13	Sequence 13, Appl1
16	686.6	58.4	1173	18	US-10-349-253A-1	Sequence 1, Appl1
17	686.6	58.4	1173	19	US-10-723-955-13	Sequence 13, Appl1
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39	172.8	14.7	2700	21	US-10-759-463-5	Sequence 5, Appl1
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44	143.2	12.2	1338	9	US-09-166-334-6	Sequence 6, Appl1
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ALIGNMENTS

RESULT 1
US-10-626-445-5
Sequence 5, Application US/10626445
Publication No. US20040248252A1
GENERAL INFORMATION:
APPLICANT: Lovenberg, Timothy
TITLE OF INVENTION: DNAS Encoding Mammalian Histamine Receptor Of The H4 Subtype
FILE REFERENCE: PRD-0032
CURRENT APPLICATION NUMBER: US/10/626,445
CURRENT FILING DATE: 2003-07-23
PRIOR APPLICATION NUMBER: 09/790,849
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 60/208,260
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 1176
TYPE: DNA
ORGANISM: Mus musculus
US-10-626-445-5

Query Match 100.0%; Score 1176; DB 20; Length 1176;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 ATGTCGAGTCTTAACAGTACTGCGATCTTGCCACAGCTGCTCAGTCCCTTGCGATT 60
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RESULT 3

US-10-626-398-5
; Sequence 5, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNA Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patencin version 3.2
; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-398-5

Query Match 100.0%; Score 1176; DB 21; Length 1176;
Beet Local Similarity 100.0%; Pred. No. 0;
Matches 1176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 6, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNA Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-445-6

Query Match 81.5%; Score 958.4; DB 20; Length 1176;
Best Local Similarity 88.4%; Pred. No. 4.3e-291;
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

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RESULT 5
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; Sequence 6, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNA Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-126-6

Query Match 81.5%; Score 958.4; DB 21; Length 1176;
Best Local Similarity 88.4%; Pred. No. 4.3e-291;
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

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DB 1 ATGTGGAGTCTTAACAGTATGTCATCTTCCACCAAGCTGCTCAGTCCCTTGGCATTT 60
QY 61 TTAATGCTCTTATGCTTCTTCTATTAATGATGAGCAATGCTGGTCACTTACCTTT 120
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Qy 901 AGAAGACTAGCCAGGCTGCTGAGCAATCTTCTGAGGCTTTGGCATTGCTGGGCTCCA 960
Db 901 AGAAGACTAGCCAGGCTGCTGAGCAATCTTCTGAGGCTTTGGCATTGCTGGGCTCCA 960
Qy 961 TACTGTCTGTTCACAAATGCTTTCAACTTACCCAGAGAGGAGGCCCAATGCGTGG 1020
Db 961 TACTGTCTGTTCACAAATGCTTTCAACTTACCCAGAGAGGAGGCCCAATGCGTGG 1020
Qy 1021 TGGTACAGATTTGCTTGGCTTACAGTGTTCATTTCACTTATTAATCCCTTTTATAC 1080
Db 1021 TGGTACAGATTTGCTTGGCTTACAGTGTTCATTTCACTTATTAATCCCTTTTATAC 1080
Qy 1081 CCTTTGTGTACAGGGGCTTCCAGAAAGGCTTTCTGGAAGATCTTTGTGTGACAAAGCA 1140
Db 1081 CCTTTGTGTACAGGGGCTTCCAGAAAGGCTTTCTGGAAGATCTTTGTGTGACAAAGCA 1140
Qy 1141 CCAGGCTGTACAGAAACAGTATCTTCTTGA 1176
Db 1141 CCAGGCTGTACAGAAACAGTATCTTCTTGA 1176

RESULT 6

us-10-626-398-6
; Sequence 6, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovendeg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNA Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-398-6
Query Match 81.5%; Score 958.4; DB 21; Length 1176;
Best Local Similarity 88.4%; Pred. No. 4,3e-291;
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;
Qy 1 ANGTGGAGCTTAAGTACGATCTGCACTGCAACGAGCTGCTGATCCCTTGGGATTT 60
Db 1 ANGTGGAGCTTAAGTACGATCTGCACTGCAACGAGCTGCTGATCCCTTGGGATTT 60
Qy 61 TTAATGCTTCAATTTGCTTGTGATATGTAAGGCAATGCTGTGATCTTAACTTT 120
Db 61 TTAATGCTTCAATTTGCTTGTGATATGTAAGGCAATGCTGTGATCTTAACTTT 120
Qy 121 GTGTGACAGAAACCTTACATGACATGAGATTAATTTTCTTAATTTGGCTATTCT 180
Db 121 GTGTGACAGAAACCTTACATGACATGAGATTAATTTTCTTAATTTGGCTATTCT 180
Qy 181 GACTTCCTGCTGGGTTTGAATTTCCATTCCTGTGATCCTGATACCTCTCAAGCTGTTAACTGG 240
Db 181 GACTTCCTGCTGGGTTTGAATTTCCATTCCTGTGATCCTGATACCTCTCAAGCTGTTAACTGG 240
Qy 241 AATTTTGAAGTGAATCTGCATGTTTGGCTCATTAAGTACTATCTTTGTGACACCGCA 300
Db 241 AATTTTGAAGTGAATCTGCATGTTTGGCTCATTAAGTACTATCTTTGTGACACCGCA 300
Qy 301 TCTGTCTACAAATATGCTCTCATTAAGTACTATCTTTGTGACACCGCA 360
Db 301 TCTGTCTACAAATATGCTCTCATTAAGTACTATCTTTGTGACACCGCA 360
Qy 361 TCTTAATAGGCTCAACACATGCTGATCATAAGATTTGCTCAAAATGGCTGTTGG 420
Db 361 TCTTAATAGGCTCAACACATGCTGATCATAAGATTTGCTCAAAATGGCTGTTGG 420
Qy 421 ATACTGGCTTTCTTGGTAATAGCCCGATGATTTCTGGCTTCAGATTTCTTGAAGAACAG 480
Db 421 ATACTGGCTTTCTTGGTAATAGCCCGATGATTTCTGGCTTCAGATTTCTTGAAGAACAG 480
Qy 481 ACGAACAACAAAGAGCTGTGAGCTGCTGCTGTTGTTACAGAGTGTACATCTCACCATTTACA 540
Db 481 ACGAACAACAAAGAGCTGTGAGCTGCTGCTGTTGTTACAGAGTGTACATCTCACCATTTACA 540
Qy 541 ATGCTCTTGAATTTCTGCTCTCTGCTCATCTGTGCTTATTTCAATGTACAGATTTAC 600
Db 541 ATGCTCTTGAATTTCTGCTCTCTGCTCATCTGTGCTTATTTCAATGTACAGATTTAC 600
Qy 601 TGGAGCTGTGAAGGCTGAGGCTCTCAGTAGGAGCCCTGAGCATGCTGATGTTCTGCACT 660
Db 601 TGGAGCTGTGAAGGCTGAGGCTCTCAGTAGGAGCCCTGAGCATGCTGATGTTCTGCACT 660
Qy 661 ACCCTTCCAGTCTTCAAGGACCTTACAGACAGAGCTGAGGCTTGGCAGACAGATTAAT 720
Db 661 ACCCTTCCAGTCTTCAAGGACCTTACAGACAGAGCTGAGGCTTGGCAGACAGATTAAT 720

QY 721 CCTGATTTGAAGAAATCAGCTGATCTGCTCACTCAGAAAGTCTTGAAAGAAAGACAGC 780
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Db 721 CCTGATTTGAAGAAATCAGCTGATCTGCTCACTCAGAAAGTCTTGAAAGAAAGACAGC 780
QY 781 ATTCCTGCTGCTTCTTAAGAGATCAATGAAACAGCAGATATCATGCTCTTCAAAGTGGTTCC 840
| | | | |
Db 781 ATTCCTGCTGCTTCTTAAAGAGATCAATGAAACAGCAGATATCATGCTCTTCAAAGTGGTTCC 840
QY 841 TTCTGGCGATCGGAAAGTCAAGCGCTTCCGCAAAAGGAGTACAGAGCTTCTCAGAGGC 900
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Db 841 TTCTGGCGATCGGAAAGTCAAGCGCTTCCGCAAAAGGAGTACAGAGCTTCTCAGAGGC 900
QY 901 AGGAAGCTAGCCAGAGCTCACTGCGCATCTTCTGAGGCGTTTGGCATTTGCTGGGCTCCA 960
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Db 901 AGGAAGCTAGCCAGAGCTCACTGCGCATCTTCTGAGGCGTTTGGCATTTGCTGGGCTCCA 960
QY 961 TACTGCTCTTCAATTTGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 1020
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Db 961 TACTGCTCTTCAATTTGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 1020
QY 1021 TGGTACAGATTTGCTTCTTCTGCTGCAATGATTCATTTCTTGTATCTCTTCTGATC 1080
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Db 1021 TGGTACAGATTTGCTTCTTCTGCTGCAATGATTCATTTCTTGTATCTCTTCTGATC 1080
QY 1081 CCTTTGTCTACAGAGCGCTTTCAGAAAGCGTTTCTGGAAGATACCTTTGTGCAAAAGCAA 1140
| | | | |
Db 1081 CCTTTGTCTACAGAGCGCTTTCAGAAAGCGTTTCTGGAAGATACCTTTGTGCAAAAGCAA 1140
QY 1141 CGAGGCTGTCAAGAACAGTCAATCTTCTTGA 1176
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Db 1141 CGAGGCTGTCAAGAACAGTCAATCTTCTTGA 1176

RESULT 7

US-09-812-216-1
; Sequence 1, Application US/09812216
; Patent No. US20020098539A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monema, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; FILE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01059
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-812-216-1

Query Match 58.4%; Score 686.6; DB 9; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2.7e-205;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTGAGATTAACAGTACTGAGCATCTTGGCCAGCGCTGACAGGCTCCCTTGGCATTT 60
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Db 1 ATGTGAGATTAACAGTACTGAGCATCTTGGCCAGCGCTGACAGGCTCCCTTGGCATTT 60
QY 61 TTAATGCTTCACTTTGCTTGTATTAATGTAAGCAATGCTGTGCTCACTTAAAGCTTT 120
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Db 61 TTAATGCTTCACTTTGCTTGTATTAATGTAAGCAATGCTGTGCTCACTTAAAGCTTT 120
QY 121 GTGGTGAAGAAAGCTTGAAGATGATTAATTTTCTTAATTTGGCTAATTTCT 180
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Db 121 GTGGTGAAGAAAGCTTGAAGATGATTAATTTTCTTAATTTGGCTAATTTCT 180
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QY 181 GACTTCTGTGGGTTGATTTCAATCTCTGATCATCTCCAGCTGTGTTAACTG 240
| | | | |
Db 181 GACTTCTGTGGGTTGATTTCAATCTCTGATCATCTCCAGCTGTGTTAACTG 240
QY 241 AATTTTGAAGTGAATCTGATGTTTGGCTCATTAATCTGATCTTTTGTGACCGCA 300
| | | | |
Db 241 AATTTTGAAGTGAATCTGATGTTTGGCTCATTAATCTGATCTTTTGTGACCGCA 300
QY 301 TCTGCTCAATATGTCCTCATTTAGTACATGATGATCCAGTCACTTCAATGCTG 360
| | | | |
Db 301 TCTGCTCAATATGTCCTCATTTAGTACATGATGATCCAGTCACTTCAATGCTG 360
QY 361 TCTTATTAAGAGTCAACACTGATCATGAAAGATTTGCTCAATGATGCTGTTGG 420
| | | | |
Db 361 TCTTATTAAGAGTCAACACTGATCATGAAAGATTTGCTCAATGATGCTGTTGG 420
QY 421 ATACTGCTTTCTTGTAAATGAGCCGATGATTTGCTGCTTCAATTTTGAAGAAC 480
| | | | |
Db 421 ATACTGCTTTCTTGTAAATGAGCCGATGATTTGCTGCTTCAATTTTGAAGAAC 480
QY 481 ACGAACAGAAAGTGAAGTGGCTGCTTGTAAAGAGTGTATCATCTCACATTTCA 540
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Db 481 ACGAACAGAAAGTGAAGTGGCTGCTTGTAAAGAGTGTATCATCTCACATTTCA 540
QY 541 ATGCTCTTGAATTTCTGCTTCTGCTGATCTCTGCTGATTTTCAATGATCAGATTTAC 600
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Db 541 ATGCTCTTGAATTTCTGCTTCTGCTGATCTCTGCTGATTTTCAATGATCAGATTTAC 600
QY 595 TCAATCTTGAATTTCTGATCCAGTCAATCTTATGCTTATTTTCAATGATTTAT 594
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Db 595 TCAATCTTGAATTTCTGATCCAGTCAATCTTATGCTTATTTTCAATGATTTAT 594
QY 601 TGAAGCTGTGAAGAGTGAAGGCTCTCAATGATGCTTCAAGCATGCTGATTTCTCACT 660
| | | | |
Db 601 TGAAGCTGTGAAGAGTGAAGGCTCTCAATGATGCTTCAAGCATGCTGATTTCTCACT 660
QY 654 TGAAGCTGTGAAGAGTGAAGGCTCTCAATGATGCTTCAAGCATGCTGATTTCTCACT 654
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Db 654 TGAAGCTGTGAAGAGTGAAGGCTCTCAATGATGCTTCAAGCATGCTGATTTCTCACT 654
QY 661 AACTCTTCAAGTCTTCAAGACATTTACAGAGCTGAGGCTGCTGAGGCAAGTAT 720
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Db 661 AACTCTTCAAGTCTTCAAGACATTTACAGAGCTGAGGCTGCTGAGGCAAGTAT 720
QY 714 GTCCTTTCACATCTGATGACATCTTCAAGAGTGAACATATCTTCAAGAGATCTCTT 714
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Db 714 GTCCTTTCACATCTGATGACATCTTCAAGAGTGAACATATCTTCAAGAGATCTCTT 714
QY 721 CCTGATTTGAAGAAATCAGCTGATCTGCTGATCTGCTGATTTTCAATGATCAGATTTAC 780
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Db 721 CCTGATTTGAAGAAATCAGCTGATCTGCTGATCTGCTGATTTTCAATGATCAGATTTAC 780
QY 745 TCTGATGACAGAAAGTCTGATCTTCACTTCACTTCACTGAGAGACAGAGAAAGTAT 774
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Db 745 TCTGATGACAGAAAGTCTGATCTTCACTTCACTTCACTGAGAGACAGAGAAAGTAT 774
QY 781 ATCTGCTGCTTAAAGATCTCAATGAAACAGCAGATATCATCTTCAAAAGGCTTCC 840
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Db 781 ATCTGCTGCTTAAAGATCTCAATGAAACAGCAGATATCATCTTCAAAAGGCTTCC 840
QY 775 CTATGATTTCTCAAGAAACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 834
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Db 775 CTATGATTTCTCAAGAAACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 834
QY 841 TTCTGGCGATCGGAAAGTGAAGCGCTTGGCCAAAGGAGTACGAGAGCTTCTGAGAGC 900
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Db 841 TTCTGGCGATCGGAAAGTGAAGCGCTTGGCCAAAGGAGTACGAGAGCTTCTGAGAGC 900
QY 894 TTCTCCATCATGATTTCTGATGCTTTCACAAAGGAAACATGTTGAATCTGTTAGAGC 894
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Db 894 TTCTCCATCATGATTTCTGATGCTTTCACAAAGGAAACATGTTGAATCTGTTAGAGC 894
QY 901 AGGAAGTGAAGCAAGTCACTGATCTGCTGATCTGATGAGCGCTTGGCCATTTGCTGAGC 960
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Db 901 AGGAAGTGAAGCAAGTCACTGATCTGCTGATCTGATGAGCGCTTGGCCATTTGCTGAGC 960
QY 954 AGGAATTAAGCAATCATCTGCGCATTTCTTAAAGGCTTTTGGCTTGGCTGCTCA 954
| | | | |
Db 954 AGGAATTAAGCAATCATCTGCGCATTTCTTAAAGGCTTTTGGCTTGGCTGCTCA 954
QY 961 TACTGCTGCTTCAATTTGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 1020
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Db 961 TACTGCTGCTTCAATTTGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 1020
QY 995 TATTCCTGCTTCAATTTGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 1014
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Db 995 TATTCCTGCTTCAATTTGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 1014
QY 1021 TGGTACAGATTTGCTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
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Db 1021 TGGTACAGATTTGCTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1074 TGGTATTAAGATGATTTGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 1074
| | | | |
Db 1074 TGGTATTAAGATGATTTGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 1074
QY 1081 CCTTTGTCTACAGAGCGTTTTCAGAAAGCGTTTCTGGAAGATACCTTTGTGCAAAAGCAA 1140
| | | | |
Db 1081 CCTTTGTCTACAGAGCGTTTTCAGAAAGCGTTTCTGGAAGATACCTTTGTGCAAAAGCAA 1140
QY 1141 CCAAGCTGTCAAGAAC---CAGTCAATCTTCTTGA 1176
| | | | |
Db 1141 CCAAGCTGTCAAGAAC---CAGTCAATCTTCTTGA 1176
QY 1195 CCTTACCATCAACAACAGTGTGAGTATCTTCTTAA 1173
| | | | |

RESULT 8

US-09-910-411-1
Sequence 1, Application US/09910411
Patent No. US20020137054A1
GENERAL INFORMATION:
APPLICANT: Bergsma, Derk
APPLICANT: Fitzgerald, Laura
APPLICANT: Li, Xiaolong
APPLICANT: Michalovich, David
APPLICANT: Zhu, Yuan
TITLE OF INVENTION: AKOR35, A G-Protein Coupled Receptor
FILE REFERENCE: GP70655-2C1
CURRENT APPLICATION NUMBER: US/09/910,411
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 09/693,761
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/497,790
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/431,898
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapien
US-09-910-411-1

Query Match 58.4%; Score 686.6; DB 9; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2,7e-205;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTGGAGCTTACAGTACGATGCGCATCTTGGCCAGCAGCTGCTCAGGTCCTCCCTTGGCATTT 60
DB 1 ATGCCAGATACATATAGCACAATCAATTAATCACTAAGACCTCGTGTACTTATAGCATTT 60
QY 61 TTAATGCTCTTCAATTTGCTTGTGATATAGTGGCAATGCTGTGCTATCTTACGCTTT 120
DB 61 TTTATGCTCTTGTACTCTTTTGTCTAATAGCTAGAAATGCTTGTGCTATTTAGCTTTT 120
QY 121 GTGGTGGAGAAACCTTACAGCATGCAAGATTAATTTTCTTAATTTGGCTATTTTC 180
DB 121 GTGGTGGAGAAACCTTACAGCATGCAAGATTAATTTTCTTAATTTGGCTATTTTC 180
QY 181 GACTTCCTGCTGCTTGTGATTTCCATCTCTGTATACCTCCCTCAGCTGTGTTAACTG 240
DB 181 GACTTCCTTGTGGGTGTGATCTTCATCTCTTGTATACCTCCCTCAGCTGTGTTAACTG 240
QY 241 AATTTTGAAGTGAATCTGCATGTTTGGCTCATTAAGTATCTTTTGTGACCGCA 300
DB 241 GATTTTGAAGAAATCTGTGATTTTGGCTCACAAGTATCTGTTATGTACAGCA 300
QY 301 TCGTCTACAAATTTGCTCATTAAGTATGATCGATGCAATGCAAGTATTCCTCAATTTG 360
DB 301 TCTGTATATACAAATTTGCTCATTAAGTATGATCGATGCAATGCAAGTATTCCTCAATTTG 360
QY 361 TCTTAATAGGCTTCAACACACTGCGATCATGAAGATTTGCTCAATAGTGTGCTTTG 420
DB 361 TCTTAATAGAACTCAACACTGCGGTCTTGAAGATTTGTAATGATGAGGCTTTG 420
QY 421 AATCTGCTTTCTTGTAAATGAGCCGATGATTTGCTTCAAGATTTTGAAGAAACAGC 480
DB 421 GTGCTGCTTCTTGTAAATGAGCCGATGATTTGCTTCAAGATTTTGAAGAAAGGA---- 476
QY 481 AGCAACAAAGAGCTGAGCTGCTTGTAAAGAGTGAATCTCCACCATTA 540
DB 477 --TGAAGTGAATGATGAATGAATCTGGAATTTTTCGAAGTGAATCTCCACCATTA 534
QY 541 ATGCTCTTGAATTTCTGCTTCTGCTCATCTGTGCTTAATTTCAATGATTAACATTTAC 600
DB 535 TCATCTTGTGAATGTGTGATCCAGTCACTTAAGTGTGCTTAATTTCAATGATTAATTT 594
QY 601 TGAAGCTTGAAGGTGAGGCTCTCAAGTGTGCTTGAAGCATGCTGATTTCTGACT 660

DB 595 TGAAGCTTGTGAAGGCTGATCATCTCAAGTGTGCTCCAAAGCATCTGCACTGCT 654
QY 661 ACCTCTTCAAGTCTTCAAGACACTTACACAGAGCTGGGTGCTTGCAGACAACTAAT 720
DB 655 GTCTCTTCAACATCTGTGAGCACTCATTTCAAGAGTAACTATCTTCAAGGATATCTTT 714
QY 721 CCTGATTTGAAGATCAAGCTGCTGCTGCTCACTCAAGAAATCTTGAAGAAAGACAGC 780
DB 715 TCTGCAATCAACAGAAATCTGCTGCTTCAATTCAGAGAGACAGAGAGAAAGATAGT 774
QY 781 ATCTGCTGCTTCAAGTCACTCAAGACAGAGATATCAAGCTTCAAGAGGCTTCC 840
DB 775 CTATGTTTCTTCAAGAAACCAAGATGAATGCAATGCTTCAAGAAATGCTTCC 834
QY 841 TTCTGCGATTCGAAAGTCAAGGCTTCCGCAAGAGAGTACGACAGCTTCAAGAGC 900
DB 835 TTCTCCATTCAGATTTCTGATGCTTCAACAGAGGAAATGTAATCTGCTTAAGCC 894
QY 901 AGAAGCTTACCAAGCTGCTGCTGCTTCTGAGGCTTTTGCATTTGCTGGGCTCA 960
DB 895 AGGAGATTAAGCCAAAGTCACTGCGCATTTCTTAAGGGGTTTGTGCTGGGCTCA 954
QY 961 TACTGCTGCTTCAAGTATGCTTCAACTTACCCAGAACGAAAGCCCAATGCTG 1020
DB 955 TATCTCTTCAACAAATGCTTCAATTTTATCTCTGAGCAACAGCTCTTAATGAT 1014
QY 1021 TGTACAGATTTGCTTGTGCTGCAATGCTTCAATTTGCTTGTATCTTCTGTAC 1080
DB 1015 TGTATAGAAATGATTTTGTGCTGAGTGTGCTTCAATCTTGTGCTATCTTGTAT 1074
QY 1081 CCTTGTGTCAAGGCTTTCAGAAAGCTTTCTGGAAGATCTTGTGTGACAAAGCA 1140
DB 1075 CATTTGTGTCAAGGCTTTCAGAAAGCTTTCTGGAAGATTTTGTGTATTAAGCA 1134
QY 1141 CCAAGGCTGTCAAGAAC--CAGTCAATCTTCTTGA 1176
DB 1135 CCTTACATCAACAAACAGTGTGCTGATCTTCTTAA 1173

RESULT 9
US-09-875-076-13
Sequence 13, Application US/09875076
Publication No. US20030017528A1
GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: AREN0050
CURRENT APPLICATION NUMBER: US/09/875,076
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 09/417,044
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,437
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,567
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,127
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,131


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; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
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; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-876-252-13

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Query Match      58.4%; Score 686.6; DB 10; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2,7e-205;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

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QY 1 ANTCGAGAGCTTAACTAGTATGTCATGTCACGAGCTGCTGAGTCCCTTGGCATTT 60
DB 1 ATGCCAGATACATATAGCAATCAATTTATCACTAAGCACTGCTTACTTTAGCATTT 60
QY 61 TTAATGCTTCATTTGCTTGGCTTATATATATATATATATATATATATATATATAT 120
DB 61 TTAATGCTTCATTTGCTTGGCTTATATATATATATATATATATATATATATATAT 120
QY 121 GTGGTGAAGAAACCTTAGACATCGAAGTAATATATATATATATATATATATAT 180
DB 121 GTGGTGAAGAAACCTTAGACATCGAAGTAATATATATATATATATATATATAT 180
QY 181 GACTTCTCTGCTGTTGATTTGATTTCTCTGACATCTCTACAGTGTGTTAACTGG 240
DB 181 GACTTCTCTGCTGTTGATTTGATTTCTCTGACATCTCTACAGTGTGTTAACTGG 240

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QY 241 AATTTGGAAGGAAATCTGCATGTTTGGCTCATTAAGTATCTTTTGGACCCGA 300
DB 241 GATTTGGAAGGAAATCTGTATTTTGGCTCATTAAGTATCTTTTGGACCCGA 300
QY 301 TCTGTCTAAGATTTTCTCTCATTAAGTATCTTTTGGCTCATTAAGTATCTTTT 360
DB 301 TCTGTCTAAGATTTTCTCTCATTAAGTATCTTTTGGCTCATTAAGTATCTTTT 360
QY 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTTGCTCAATATGCTGTTGG 420
DB 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTTGCTCAATATGCTGTTGG 420
QY 421 ATACGCTCTTCTTGTAAATGAGCCGATGATTTGCTTCAATTTCTTGAAGAAC 480
DB 421 ATACGCTCTTCTTGTAAATGAGCCGATGATTTGCTTCAATTTCTTGAAGAAC 480
QY 481 AGCAACAAAGAACTGTGAGCTGCTTGTTCAGAGTGTGATCTTCTCAACATTA 540
DB 481 AGCAACAAAGAACTGTGAGCTGCTTGTTCAGAGTGTGATCTTCTCAACATTA 540
QY 541 ATGCTCTTGAATTTCTGCTTCTGTCATCTGTGCTTATTTCAATGATACAGATT 600
DB 541 ATGCTCTTGAATTTCTGCTTCTGTCATCTGTGCTTATTTCAATGATACAGATT 600
QY 601 TGAAGCTGTGAAGAGGCTCTCAGTATGCTGCTTGAAGCTGATTTCTCACT 660
DB 601 TGAAGCTGTGAAGAGGCTCTCAGTATGCTGCTTGAAGCTGATTTCTCACT 660
QY 661 ACCTCTTCAAGCTCTCAGACATTAACACAGAGCTGCTGCTGACAGACATTA 720
DB 661 ACCTCTTCAAGCTCTCAGACATTAACACAGAGCTGCTGCTGACAGACATTA 720
QY 721 CTTGATTTGAAGATCAGCTGATCTGCTCACTCAGAAAGTCTGAAAGAGACAG 780
DB 721 CTTGATTTGAAGATCAGCTGATCTGCTCACTCAGAAAGTCTGAAAGAGACAG 780
QY 781 ATCTGTGTCTTAAAGATCAATGAACAGATGATCACTGCTTCAAGTGGTTC 840
DB 781 ATCTGTGTCTTAAAGATCAATGAACAGATGATCACTGCTTCAAGTGGTTC 840
QY 841 TTTGAGCATCGAAAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 841 TTTGAGCATCGAAAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 AGGAGCTAGCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 901 AGGAGCTAGCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 TACTGTCTGCTCAATTTGCTTCACTTCACTTCACTTCACTTCACTTCACTTCA 1020
DB 961 TACTGTCTGCTCAATTTGCTTCACTTCACTTCACTTCACTTCACTTCACTTCA 1020
QY 1021 TGGTACAGATTTGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1021 TGGTACAGATTTGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1081 CTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1081 CTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1141 CCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1176
DB 1141 CCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1176
QY 1176 CTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1240
DB 1176 CTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1240

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RESULT 11
US-10-052-193-1
; Sequence 1, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A

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; CURRENT APPLICATION NUMBER: US/10/052,193
 ; CURRENT FILING DATE: 2002-01-17
 ; PRIOR APPLICATION NUMBER: 0101223.6
 ; PRIOR FILING DATE: 2001-01-17
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 1173
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-052-193-1

Query Match 58.4%; Score 686.6; DB 13; Length 1173;
 Best Local Similarity 75.1%; Pred. No. 2.7e-205;
 Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

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QY 1 ATGTGGAGTCTTAAGTGAAGTCTGAGTCTGCGACGCGCTGCGAGGTCCCTGGAGATT 60
DB 1 ATGCCAGATCTAATAGCAACAATCAATTAATCACTAGACATCGTGTACTTTAGCAATT 60
QY 61 TTAATGCTCTTCAATTTGCTTGTCTAATAGTAAAGCAATGCTGTGCTTACCTTAC 120
DB 61 TTTATGCTCTTGTACTCTTTGCTAATAGTAAAGCAATGCTGTGCTTACCTTAC 120
QY 121 GTGGTGAACAAGAACTTGAACATGCAAGTAATTTTCTTAAATTTGGCTATTCT 180
DB 121 GTGGTGAACAAGAACTTGAACATGCAAGTAATTTTCTTAAATTTGGCTATTCT 180
QY 121 GACTTCCTGCTGGGTTGATTTCCATCTCTGTACATCCCTCAGCTGTTTAACTGG 240
DB 181 GACTTCTTGTGGGTGATCTCTCATCTTGTGATACCTCTCAGCTGTTTAACTGG 240
QY 241 AATTTTGAAGTGAATCTGCAATGTTTGGCTCATCTTACTATCTTTTGTGACCGCA 300
DB 241 GATTTTGAAGGAATCTGTGATTTTGGCTCATCTGATCTGTTATGTACAGA 300
QY 301 TCTGTCTAATATTTGCTCTCATTTAGCTACATGATACCAAGTCAAGTTTCAATGCT 360
DB 301 TCTGTATATTAATATTTGCTCTCATCTGATGATGATGATGATGATGATGATGAT 360
QY 361 TCTTATAGAGCTCAACATGATGATGATGATGATGATGATGATGATGATGATGAT 420
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QY 421 ATACTGCTCTTCTTGTGTAATGAGCCGATGATTTGCTGCTTCAAGATCTTGAAGA 480
DB 421 GTGCTGCTCTTCTTGTGTAATGAGCCGATGATTTGCTGCTTCAAGATCTTGAAGA 480
QY 481 AGGAACAACAAGAGCTGAGCTGAGCTGCTTTGTAACAAGTGTACTCTCAACATTACA 540
DB 477 --TGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 534
QY 541 ATGCTCTTGAATTCCTGCTCTCTGATCTCTGCTGCTTATTTCAATGATGATGAT 600
DB 535 TCATTTTGAATTCCTGATTCAGTCACTTATGCTTATTTCAACATGATGATGAT 594
QY 601 TGAAGCTTGAAGAGCTGAGCTGCTCAGTGAAGTGCCTTACGCAATGCTGATCTCACT 660
DB 595 TGAAGCTTGAAGAGCTGATATCTCAATGAGTGCCTTACGCAATGCTGATCTCACT 654
QY 661 ACTCTTCAAGTCTTCAAGACATTAACAACAAGCTGAGCTGCTTGAACAAGTAAT 720
DB 655 GTCTCTTCAACAATCTGTGACATCTATTCAGAGGATGATCTTCAAGAGATCTCT 714
QY 721 CCGATTTGAAGGAATCAGTGTATCTGTCACTCAAGAAAGTCTGAGAAAGAGCAGC 780
DB 715 TCTGATCTCAACAAGATCTCTGATCTTCTTCACTCAAGAAAGAGAGAGAGTACT 774
QY 781 ATCTGCTGCTCTTGAAGATCAATGAACAGAGATATCACTGCTTCAAGTGGCTTCC 840
DB 775 CTCATGTTTCTCTCAAGAAACAAGATGATGATGATGATGATGATGATGATGATGAT 834
QY 841 TTTGCGCATCGGAAGATGAGCGCTTCCCAAGGAGATGACGAGAGCTTCTCAGAGGC 900
  
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DB 835 TTCTCCCATCAAGATCTGTACTCTTCAACCAAGGAACAATGTGATGCTTTAGAGCC 894
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DB 895 AGGAAGTACAGCAGGCTGAGCTGATCTCTTGAAGGCTTTGGCAATTTGCTGGCTCA 954
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QY 1021 TGTACAGATTTGCTGCTGCTGCAATGCTTCAATGCTTGTATTCCTTCTGATC 1080
DB 1015 TGTATAGATTTGCTGCTGCTGCAATGCTTCAATGCTTGTATTCCTTCTGATC 1074
QY 1081 CTTTGTGCAAGGCTTTCAGAGGCTTTCAGAGGCTTTCAGAGGCTTTCAGAGGCT 1140
DB 1075 CCATTTGCTCAAGGCTTTCAGAGGCTTTCAGAGGCTTTCAGAGGCTTTCAGAGGCT 1134
QY 1141 CCAGGCTGCTCAAGAGC--CAGTCAATGCTTCTGA 1176
DB 1135 CCTTACCATCAACAACAGTGTGATCTTCTTAA 1173
  
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RESULT 12
US-10-272-983-13
; Sequence 13, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-983-13

Query Match 58.4%; Score 686.6; DB 15; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2.7e-205;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;
  
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QY 61 TTAATGCTTCATTTGCTTGTCTATTAATGAGGCAATGCTGTGATCTTAAGCTTT 120
 DB 61 TTTATGCTCTTGTAGTCTTTTGTCTATTAATGCTAGGAATGCTTTGCTATTTAGCTTT 120
 QY 121 GTGGTGGACAGAAACCTTGAACATCGAATTAATTTTCTTAATTTGGCTAATTTCT 180
 DB 121 GTGGTGGACAGAAACCTTGAACATCGAATTAATTTTCTTAATTTGGCTAATTTCT 180
 QY 181 GACTTCTGTGGGTTGATTTCCATTCCTGTGATACCTCTACAGGTTGTTTAATCTG 240
 DB 181 GACTTCTGTGGGTTGATTCCTGTGATACCTCTGTGATACCTCTACAGGTTGTTTAATCTG 240
 QY 241 AATTTTGAAGTGAATCTGCATGTTTGGCTCATTAAGTATCTTTTGTGACACGCA 300
 DB 241 GATTTTGAAGGAATCTGTGATTTTGGCTCATTAAGTATCTTTTGTGACACGCA 300
 QY 301 TCTGTCTCAATATTGTCTCATTAAGTATGATGATGATGATGATGATGATGATGATG 360
 DB 301 TCTGTATTAATTAATGCTCTCATTAAGTATGATGATGATGATGATGATGATGATG 360
 QY 361 TCTTATAGGGCTCAACATCTGCATCAATGATGATGATGATGATGATGATGATGATG 420
 DB 361 TCTTATAGAACTCAACATCTGCATCAATGATGATGATGATGATGATGATGATGATG 420
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 DB 421 GTGCTGGCTTTCTTGTGTAATGAGCCGATGATTTCTGGCTTCAGATTTCTTGAAGAACAGC 480
 QY 481 ACGAACAACAAAGACTGTGAGCTGTGCTTTGTTACAGAGTGTGATCATCTCACATTTACA 540
 DB 477 --TGAAGTAGTAAGTGAACCTGGATTTTTCGGAATGTGATACCTTGGCATACACA 534
 QY 541 ATGCTCTTGAATTCCTGCTTCTGTGATCTGTGCTTATTTCAATGATGATGATGATGATG 600
 DB 535 TCATTTTGAATTCGTGATCCAGTATCTTGAATGATGATGATGATGATGATGATGATG 584
 QY 601 TGGAGCTGTGGAAGGTGAGGCTCTCAGTATGCTGCTGATGCTGATTTCTGCACT 660
 DB 595 TGGAGCTGTGGAAGGTGATATCATCTCAGTATGCTGCAAGCAATCTGATGATGATG 654
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 DB 655 GTCTCTTCAACATCTGTGACACTCATCTCAGAGTATGATCTTCAAGAGATCTCTT 714
 QY 721 CCTGATTAAGGAATCAGTGTGATCTGCTCATCTCAGAAAGTCTCTGGAAGAAAGACAGC 780
 DB 715 TCTGATGACACAAAGTCTGTGATCTTTCATTTCAAGAGACAGAGAAAGAGATGAT 774
 QY 781 ATCTGTGTCTTAAAGACTCAGATGATCAGAGATGATCAGTCTTCAAGTGGGTTTC 840
 DB 775 CTGATGTTTCTTCAAGAAACAGATGATGATGATGATGATGATGATGATGATGATG 834
 QY 841 TTCTGGCATCGGAAGTGAAGGCTTCCGCAAGAGAGTACAGAGCTTCTCAGAGC 900
 DB 835 TTCTCCCAATCAGATCTGTGATCTTCAACAAAGGACATGTTGAATCTTGAAGCC 894
 QY 901 AGGAAGTGAAGGCTGATCTGAGGCTTCTGAGGCTTTTGGCATTTGCTGGGCTCCA 960
 DB 895 AGGAAGTGAAGGCTGATCTGAGGCTTCTGAGGCTTTTGGCATTTGCTGGGCTCCA 954
 QY 961 TACTGTCTGTCAATTTGCTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCA 1020
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 QY 1021 TGGTACAGATGCTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1080
 DB 1015 TGGTATAGAAATGCTATTTGGCTTCAAGTGTGATGATGATGATGATGATGATGATG 1074
 QY 1081 CCTTTGTGTCAAGGGCTTCTCAGAGGCTTTTGTGAAGTATCTTTGTGAGAACAGCA 1140
 DB 1075 CCAATGTGTCAAGGGCTTCTCAGAGGCTTTTGTGAAGTATTTGTATTAATAAAGCA 1134

QY 1141 CCAGCGCTGTACAGAAC---CAGTCAGTATCTTCTTGA 1176
 DB 1135 CCTTACATCAACACAGAGTGGTCAATCTTCTTAA 1173
 RESULT 13
 US-10-354-769-1
 ; Sequence 1, Application US/10354769
 ; Publication No. US20030149242A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pfizer Inc.
 ; APPLICANT: O'Reilly, Mark A.
 ; APPLICANT: Peter, Beate
 ; TITLE OF INVENTION: NOVEL POLYPEPTIDE
 ; FILE REFERENCE: PC10373B
 ; CURRENT APPLICATION NUMBER: US/10/354,769
 ; CURRENT FILING DATE: 2003-01-30
 ; PRIOR APPLICATION NUMBER: US 09/698,801
 ; PRIOR FILING DATE: 2000-10-27
 ; PRIOR APPLICATION NUMBER: US 60/211,243
 ; PRIOR FILING DATE: 2000-06-14
 ; PRIOR APPLICATION NUMBER: GB 9925641.4
 ; PRIOR FILING DATE: 1999-10-29
 ; PRIOR APPLICATION NUMBER: GB 0009973.9
 ; PRIOR FILING DATE: 2000-04-20
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 1173
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-354-769-1
 Query Match 58.4%; Score 686.6; DB 15; Length 1173;
 Best Local Similarity 75.1%; Pred. No. 2.7e-205;
 Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;
 QY 1 ATGCGAGATCTTAACAGTACTGATCTTGCACACAGCTGCTGAGTCCCTTGGCATTT 60
 DB 1 ATGCCAGATATCTTAATGACAAATCAATTAATCACTAAGACACTGCTTATTTAGCATTT 60
 QY 61 TTAATGCTTCATTTGCTTGTCTATTAATGATGAGCAATGCTGTGATCAATTTAGCTTT 120
 DB 61 TTTATGCTCTTGTAGTCTTTTGTCTATTAATGATGAGAAATGCTTGGTCAATTTAGCTTT 120
 QY 121 GTGGTGGACAGAAACCTTGAACATCGAATTAATTTTCTTAATTTGGCTAATTTCT 180
 DB 121 GTGGTGGACAGAAACCTTGAACATCGAATTAATTTTCTTAATTTGGCTAATTTCT 180
 QY 181 GACTTCTGTGGGTTGATTTCCATTCCTGTGATACCTCTACAGGTTGTTTAATCTG 240
 DB 181 GACTTCTGTGGGTTGATTCCTGTGATACCTCTGTGATACCTCTACAGGTTGTTTAATCTG 240
 QY 241 AATTTTGAAGTGAATCTGCATGTTTGGCTCATTAAGTATCTTTTGTGACACGCA 300
 DB 241 GATTTTGAAGGAATCTGTGATTTTGGCTCATTAAGTATCTTTTGTGACACGCA 300
 QY 301 TCTGTCTCAATATTGTCTCATTAAGTATGATGATGATGATGATGATGATGATGATG 360
 DB 301 TCTGTATTAATTAATGCTCTCATTAAGTATGATGATGATGATGATGATGATGATG 360
 QY 361 TCTTATAGGGCTCAACATCTGCATCAATGATGATGATGATGATGATGATGATGATG 420
 DB 361 TCTTATAGAACTCAACATCTGCATCAATGATGATGATGATGATGATGATGATGATG 420
 QY 421 ATACTGGCTTTCTTGTGTAATGAGCCGATGATTTCTGGCTTCAGATTTCTTGAAGAACAGC 480
 DB 421 GTGCTGGCTTTCTTGTGTAATGAGCCGATGATTTCTGGCTTCAGATTTCTTGAAGAACAGC 480
 QY 481 ACGAACAACAAAGACTGTGAGCTGTGCTTTGTTACAGAGTGTGATCATCTCACATTTACA 540
 DB 477 --TGAAGTAGTAAGTGAACCTGGATTTTTCGGAATGTGATACCTTGGCATACACA 534

QY	541	ATGCTCTGGAAATTCCTGCTCTGTCATCTCGTGGCTTAATTCAAATGACAAATTC	600
Db	535	TCATTCCTGGAAATGCTGATCCAGATCATCTTAGTCCTTAATTCACATGAATATTAT	594
QY	601	TGAGACCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTAGCCATCTGGATTCCTCACT	660
Db	595	TGGACCTGTGGAAGGTGATCATCTCACTAAGGTGCCAAGCATCTTGGACTGATGGCT	654
QY	661	ACCTCTTCCAGTCTTCAGAGACCTTACACACAGCTGGGGTGGCTTCAGACACAGTAAT	720
Db	655	GTCTCTTCCAAATCTGTGGAACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCT	714
QY	721	CCTGATTTGAAGAAATCAGCTGCATCTGCTACCTCAGAAAGTCTCGAAGAAAGACACAG	780
Db	715	TCTGATTCACAGAAATCTCTGCATCTTTCATTCAGAGAGACAGAGAGAAAGATAGT	774
QY	781	ATCTGCTGTCTCTTAAGACTCACATGAAACAGAGATACACTGCTTCAAGTGGGTCC	840
Db	775	CTCATGTTTTCCTCAAGAACCAAGATGAATAGCAATTCCTCCAAATGGGTTCC	834
QY	841	TTCTGGCGATCGGAAAGTGACAGCGCTTGGCCAAAGGAGTACGACAGGCTTCTCAGAGGC	900
Db	835	TTCTCCCAATCAGATTCGTAGCTCTTTCACAAAGGGAACATGTTGAATGCTTAGAGCC	894
QY	901	AGGAAGCTAGCCAGGTCATCTGGCCATCTTCTGAGGCTTTTGCCATTTGCTGGGCTCA	960
Db	895	AGGAATATTAGCCAAAGTCACTGGCCATCTCTTAAGGGGTTTTGTGCTTGGGGCTCCA	954
QY	961	TACTGCTGTGTCACAATTTGCTCTTCAACTTACCCAGAACGGAAAGCCCAATCGGTG	102
Db	955	TATTCCTGTTCACAAATGTCTCTTTCATTTTATCTCAGCAACAGGCTCTTAATCAGTT	101
QY	1021	TGGTACAGCATTCCTTCTGGGTGCATAGGTTCAATTCGTTGTATATCCCTTCTGTAC	108
Db	1015	TGGTATAGAAATTGCAATTTGGGCTTGAGGTTCATTTCTTGTCAATCTCTTTGTAT	107
QY	1081	CCTTGTGTGCACAGGCGTTTCCAGAAAGGCTTTCTGGAAGATCTTGTGTGACAAAGCA	114
Db	1075	CCATTGTGTCAACACGCGCTTTCAAAAAGGCTTTCTGAAAAATTTTGTATAAAAAGCAA	113
QY	1141	CCAGCGCTGTCAACAGAAC--CAGTCAGTATCTTCTTGA	1176
Db	1135	CCTTACATCAACAACACAGTGGGTGATCTTCTTAA	1173
RESULT 14			
US-10-393-807-13			
Sequence 13, Application US/10393807			
Publication No. US20030175891A1			
GENERAL INFORMATION:			
APPLICANT: Chen, Ruoping			
APPLICANT: Dang, Huang T.			
APPLICANT: Liaw, Chen W.			
APPLICANT: Lin, I-lin			
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors			
FILE REFERENCE: AREN0050			
CURRENT APPLICATION NUMBER: US/10/393, 807			
CURRENT FILING DATE: 2003-03-21			
PRIOR APPLICATION NUMBER: US/09/417, 044			
PRIOR FILING DATE: 1999-10-12			
PRIOR APPLICATION NUMBER: 60/109, 213			
PRIOR FILING DATE: 1998-11-20			
PRIOR APPLICATION NUMBER: 60/120, 416			
PRIOR FILING DATE: 1999-02-16			
PRIOR APPLICATION NUMBER: 60/121, 851			
PRIOR FILING DATE: 1999-02-26			
PRIOR APPLICATION NUMBER: 60/123, 946			
PRIOR FILING DATE: 1999-03-12			
PRIOR APPLICATION NUMBER: 60/123, 949			
PRIOR FILING DATE: 1999-03-12			
PRIOR APPLICATION NUMBER: 60/136, 436			
PRIOR FILING DATE: 1999-05-28			
PRIOR APPLICATION NUMBER: 60/136, 437			

[illegible]

QY 841 TTCTGGCGATCGGAAGTGCAGCGCTTCGCCAAAGGAGTACGAGCTTCTCAGAGGC 900
DB 835 TTCTCCCAATCAGATTCTGTAGCTCTTCAACCAAGGAAACATGTGAATGCTTAAAGCC 894
QY 901 AGGAGCTAGCCAGGTCACTGCGCATCTCTTGAGCGCTTTGCCATTTGCTGAGCTCA 960
DB 895 AGGAGATTAGCCCAAGTCACTGCGCATCTCTTGAGCGCTTTGCTGAGCTTCA 954
QY 961 TACTGTCTGTCAATGTGCTTTCACTTACCCCAAGAGCGCCCAATGCGTG 1020
DB 955 TATCTCTGTTCACAAATGTCTTTCAATTTATTCCTGACCAAGCTCTCAATCAAGTT 1014
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QY 1141 CCAAGCGCTGTACAGAAC---CAGTCAATCTTTCTTGA 1176
DB 1135 CCTTACCAATCAACAGACAGTGGTCAATCTTTCTTAA 1173

RESULT 15
US-10-417-820A-13
Sequence 13, Application US/10417820A
Publication No. US20030229216A1
GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
APPLICANT: Liaw, Chen W.
APPLICANT: Lowitz, Kevin
APPLICANT: Chalmers, Derek T.
TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
FILE REFERENCE: 7.US28.CON
CURRENT APPLICATION NUMBER: US/10/417, 820A
CURRENT FILING DATE: 2003-04-16
PRIOR APPLICATION NUMBER: 09/416, 760
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 09/170, 496
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/110, 060
PRIOR FILING DATE: 1998-11-27
PRIOR APPLICATION NUMBER: 60/120, 416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121, 852
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/109, 213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/123, 944
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123, 945
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123, 948
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123, 951
PRIOR FILING DATE: 1999-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 155
SOFTWARE: PatentIn version 3.2
SEQ ID NO 13
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapiens
US-10-417-820A-13

Query Match 58.4%; Score 686.6; DB 17; Length 1173;
Best Local Similarity 75.1%; Prid. No. 2, 7e-205;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTGGAGTCTTACAGTACTGCGCATCTTGGCACAGCTGCTCAGGTCCTTGGCATTT 60
DB 1 ATGCCAGATATCTAATGACAAATCAATATTAATCACTAAGCACTGCTGTACTTAAAGATTT 60
QY 61 TTAATGTCTTCAATTTGCTTGTATTAATGTAAGGAATGCTGTGATCTTAAAGCTTT 120
DB 61 TTAATGTCTTGTACTTTTGTATTAATGCTTAATGCTTAATGCTTAAAGCTTT 120
QY 121 GGTGTGACAGAAACCTTGAACATGCAATTAATATTTTCTTAATTTGGCTATTTCT 180
DB 121 GGTGTGACAGAAACCTTGAACATGCAATTAATATTTTCTTAATTTGGCTATTTCT 180
QY 181 GACTTCTGTGAGGCTTGAATTTTCATTTCTCTGTATCATCCCTCAGCGTGTAACTGG 240
DB 181 GACTTCTGTGAGGCTTGAATTTTCATTTCTCTGTATCATCCCTCAGCGTGTAACTGG 240
QY 241 AATTTTGAAGTGAATCTGCATGTTTGGCTTCAATTAAGTACTATCTTTTGTGACCGCA 300
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DB 301 TCTGTATTAATTAACATTTGCTCTCATTTAGCTAATGATTCATACAGTCACTTTCAATGCTGTG 360
QY 361 TCTTATAGGAGCTCAACACATGCGCATGAAAGATTTGCTCAAAATGAGGCTGTTTG 420
DB 361 TCTTATTAATTAACATTTGCTCTCATTTAGCTAATGATTCATACAGTCACTTTCAATGCTGTG 420
QY 421 ATACTGCTTTCTTGTGTAATGAGCCGATGATTTGCTTCAATTTCTTGAAGAAACAGC 480
DB 421 GGTGCTGCTTCTTGTGTAATGAGGCGCAATGATTTCTTGAAGAAACAGC----- 476
QY 481 AGCAACAAAGGACGTGAGCTGCTTTGTAAGAGTGTGATCTTCAACATTAACA 540
DB 477 --TGAAGTGAAGTGAATGTAACCTGATTTTTCGAAATGTAACCTTGTGCATCAACA 534
QY 541 ATGCTTGTGAATTTCTGCTTCCTGATCTGCTGCTTAAATTTCAATGACATGATTAAC 600
DB 535 TCAATTTTGAATTTCTGATTCCTGATCTTAAATTTCAATGATTAATTAAT 594
QY 601 TGGAGCTGTGAAGGCTGAGGCTCTCAGTAGTGCTTCAAGCATGCTGATTTCTTCACT 660
DB 595 TGGAGCTGTGAAGGCTGATATCATCTCAGTAGTGCTTCAAGCATGCTGATTTCTTCACT 654
QY 661 ACTCTTTCAGTGTCTTCAAGACATTAACACAGAGCTGAGGCTTTCAGACATTAAT 720
DB 655 GTCTCTTTCAGACATCTGTGACATCACTTCAAGAGTGAATCTTCAAGAGATCTTCT 714
QY 721 CCTGATGAAGAAATCAGCTGATCTGCTCACTCAAGAAAGTCTGAAAGAAAGACAGC 780
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QY 901 AGGAGCTAGCCAGGTCACTGCGCATCTCTTGAGCGCTTTGCCATTTGCTGAGCTCA 960
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DB 955 TATCTCTGTTCACAAATGTCTTTCAATTTATTCCTGACCAAGCTCTCAATCAAGTT 1014
QY 1021 TGGTACAGATTGCTTGTGCTGCAATGCTTCAATGCTTTGTAATCCCTTTCTGTAC 1080
DB 1015 TGGTATAGAAATGCAATTTGGCTTCAGTGGTTCAATTCCTTTGCAATCCTCTTTGTAT 1074

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Qy 1081 CCTTGTGTCAAGGCGTTTCCAGAAAGCTTCTGGAAGATACTTGTGTGACAAAGCAA 1140
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Qy 1141 CGAGGCGTGTCAAGAAC---CAGTCAGTATCTTCTTGA 1176
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Db 1135 CCTTACATCAACACACAGTCGTCAGTATCTTCTTAA 1173
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Search completed: October 8, 2005, 04:43:12
Job time : 967 secs

Db 1 ATGCCAGATCTAATAGCAATCAATTTATCACTAGACCTCGTGTACTTTAGCATTT 60
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTTATGTCCTTACTAGCTTTTGTCTATATAGCTAGAAATGCTTTGGTCAATTTAGCTTT 120
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGAGCAAAAACCTTAGACATCAAGATGTAATTTTCTTAATCTGGCCATCTCT 180
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
Db 181 GACTTCTTTGGGGGAGATCTCATCTCTTGTATACATCTCTACACGCTGTCAGATGG 240
Qy 81 AsnPheGlySerGlyIleCysMetPheTyrPheLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGAAATCTGTATTTTGGCTCAGTACAGTACATCTGTATATGTAACGA 300
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATATACATCTGCTCATACAGCTATGATCGATACCTGTCAGTCCAATGCTGTG 360
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetCysIleValAlaGlnMetValAlaValTyr 140
Db 361 TCTATATAGAACTCAACATCTGGGGGCTTGAAAGATGTAATCTCTGATGGCCGTTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrPheAsnSer 160
Db 421 GTGCTGGCTCTTCTTATGATGATGGCCAAATGATTTCTATGATTCAGAGCTTGGAAAGATGA 480
Qy 161 ThrAsnThrLysAspCysGlnProGlyPheValThrGlnTyrTyrIleLeuThrIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGAAATGGTGAATCCTTGCCATCACA 534
Qy 181 MetLeuLeuGlnPheLeuLeuProValIleSerValAlaTyrPheAsnAlaGlnIleTyr 200
Db 535 TCATCTTGGAAATCTGTATCCAGATCACTTAGTGTCTTATTTCAACAATATTTAT 594
Qy 201 TTPSerLeuTyrLysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db 595 TGGAGCTGTGGAAAGGTGATCATCTCAATAGGTGCAAAAGCATCTTGACATGATGCT 654
Qy 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 655 GTCCTCTTCCAACTCTGTGACATCTCATTCAGAGGTAGACATCTTCCAAAGCATCTCT 714
Qy 241 ProGlyLeuLysGlnSerAlaIleAspArgHisSerGlnSerProArgArgLysSerSer 260
Db 715 TCTGCATCGACAAAGATCTCTGCATCTCTTCAATTCAGAGACAGAGGAGAAAGATAGT 774
Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
Db 775 CTCATGTTTTCCTCAAGAACCAAGATGATAGCAATCAATGCTTCCAAAATGGGTTCC 834
Qy 281 PheTyrArgSerGlnSerAlaIleLeuArgGlnArgGlnTyrAlaGlnLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATCTCTAGCTCTTCCACCAAGGAGCAATGTGAATGCTTTAGAGCC 894
Qy 301 ArgLysLeuValArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTyrPheLys 320
Db 895 AGGAGATTATAGCCAGATCTGGCATCTCTTATGGGGGTTTGTGCTGTGGGCTTCCA 954
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGlnArgProLysSerVal 340
Db 955 TATTCCTGCTTCAACATTTGCTTTATTTATTCCTCAGCAACAGTCTTAAATCAGTT 1014
Qy 341 TrrPlyrSerIleAlaPheTyrLeuGlnTyrPheAsnSerPheValAsnProPheLeuTyr 360
Db 1015 TGGTATAGAAATGCAATTTGGGCTTCAGTGTCAATTCCTTGTCAATCTCTTTTGTAT 1074
Qy 361 ProLeuCysHisArgArgPheGlnLysValaPheTyrPheIleLeuCysAlaThrLysTyr 380
Db 1075 CCATTTGTGTCAACAGGCTTTCAAAAAGGCTTTCTTGAATAATATTTTGTATAAAAAGCAA 1134

Qy 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
Db 1135 CCTTACCATCAACAACAGTGGTCAATCTTCT 1170

RESULT 2

US-09-812-216-1
/ Sequence 1, Application US/09812216
/ Patent No. 6613533
/ GENERAL INFORMATION:
/ APPLICANT: Behar, Jiang Xu
/ APPLICANT: Hedrick, Joseph A.
/ APPLICANT: Laz, Thomas W.
/ APPLICANT: Monama, Frederick J. Jr.
/ APPLICANT: Morse, Kelley L.
/ APPLICANT: Umland, Shelby P.
/ APPLICANT: Wang, Suke
/ TITLE OF INVENTION: Histamine receptor
/ FILE REFERENCE: CN01069
/ CURRENT APPLICATION NUMBER: US/09/812,216
/ CURRENT FILING DATE: 2001-03-19
/ PRIOR APPLICATION NUMBER: 09/414,010
/ PRIORITY FILING DATE: 1998-10-07
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 1173
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-812-216-1

Alignment Scores:

	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
US-10-626-445-8 (1-391) x US-09-812-216-1 (1-1173)	1	1370.50	78.32%	68.11%	66.92%	1173	267	40	82	3	2

Qy 1 MetSerGlnSerAsnSerThrGlyIleLeuProPheAlaIleGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATCTAATAGCAATCAATTTATCACTAGACCTCGTGTACTTTAGCATTT 60
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTTATGTCCTTACTAGCTTTTGTCTATATAGCTAGAAATGCTTTGGTCAATTTAGCTTT 120
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGAGCAAAAACCTTAGACATCAAGATGTAATTTTCTTAATCTGGCCATCTCT 180
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
Db 181 GACTTCTTTGGGGGAGATCTCATCTCTTGTATACATCTCTTCCAAAGCATCTCTTGAATGG 240
Qy 81 AsnPheGlySerGlyIleCysMetPheTyrPheLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGAAATCTGTATTTTGGCTCAGTACAGTACATCTGTATATGTAACGA 300
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATATACATCTGCTCATACAGCTATGATCGATACCTGTCAGTCCAATGCTGTG 360
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetCysIleValAlaGlnMetValAlaValTyr 140
Db 361 TCTATATAGAACTCAACATCTGGGGCTTGAAAGATGTAATCTCTGATGGCCGTTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrPheAsnSer 160
Db 421 GTGCTGGCTCTTCTTATGATGATGGCCAAATGATTTCTATGATTCAGAGCTTGGAAAGATGA 480


```

OY      284  SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294
           :: |||||::|||::|||::|||
Db      1273  GCGTCTCGGCTCTACTGAGAGAGCGCATGAAATGATGTCTCCAAAGCTTCACCCAGGCG 1333
OY      295  AlaGluLeuLeuArgGlyArgIysLeuAlaArgSerLeuAlaIleLeuSerAlaPhe 314
           |||||
Db      1333  TTTCCGCTGTCTCGGAGACAGGAAATGGCCAAAGTCGTCGCGCATGTGAGCATCTTT 1392
OY      315  AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
           ::|||::|||::|||::|||::|||::|||::|||::|||
Db      1333  GGGCTCTGTGGGCCCCAATACAGCTGCTGATGATCATCTCGGGCGCTCCCATGGCCAC 1455
OY      335  GluArgProIysSerValTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPhe 354
           |||||
Db      1453  TGGCGTCCCT---GACTACTGGTAGCAAAACCTCTCTGTGGCTCTGTGGGCAACTCGGCT 1509
OY      355  ValAsnProPheLeuTyrTrpLeuCysHisArgArgPheGlnIlyAlaPheTrpIlySile 374
           |||||
Db      1510  GTCAACCTGTCCTTACCTCTGTGACACACACACAGCTTCGCGCGGGCTTCACCAAGCTG 1563
OY      375  LeuCysValThrIle-----ProAlaLeuSerGlnAsnGlnSer 388
           |||||
Db      1570  CTGTGCCCCCAGAACTCAAAAATCCAGCCCCACAGCTCCCTGGAGACACTGCTGGAAGTGA 1622
OY      381  -----
Db      1630  GTGGGCCACAGAGCTCCCTTCAGCCAGCGCTCTCTGAGCCAGGTCT 1677

RESULT 4
US-08-985-090-1
/ Sequence 1, Application US/08985090
/ Patent No. 5885893
/ GENERAL INFORMATION:
/ APPLICANT: Andrew D. J. Goodearl
/ TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
/ NUMBER OF SEQUENCES: 28
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: LAHIVE & COCKFIELD, LLP
/ STREET: 28 State Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/985,090
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Jean M. Silverl
/ REGISTRATION NUMBER: 39,030
/ REFERENCE/DOCKET NUMBER: MN1-032
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617)227-7400
/ TELEFAX: (617)742-4214
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2689 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 291..1625
US-08-985-090-1

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Alignment Scores:		4.87e-65	length:	2689
Pred. No.:	724.50	Matches:	171	
Score:	48.90%	Conservative:	52	
Percent Similarity:	37.50%	Mismatch:	118	
Best Local Similarity:	35.38%	Indels:	115	
Query Match:		Gaps:	12	
DB:	2			
US-10-626-445-8 (1-391) x US-08-985-090-1 (1-2689)				
QY	18	LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIle	37	
DB	399	CTGGCCGGCTCATGAGCCCTCTCATCTGAGCCACGGCTGGGACACGGCTGATCATG	458	
QY	38	LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu	57	
DB	459	CTTCGCTTCGTGGCCGACCTCGAGCTCCGACCCAGAAACAATTCTTCTGCTCACTC	518	
QY	58	AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValIleu	77	
DB	519	GCCATCTTCGACTTCTCTGCGGGCCCTTGACATCCCATGTATGATACCTCACTGCTG	578	
QY	78	Phe---AsnTyrAsnPheGlySerGlyIleCysMetPheTyrPheLeuIleThrAspTyrIleu	96	
DB	579	ACAGCCGCTGACCTTCGCGCGGGCCCTTGACAGCTGAGCTGTGATGACTACCTG	638	
QY	97	LeuCysThrAlaSerValTyrAsnIleValIleIleSerTyrAspArgTyrGlnSerVal	116	
DB	639	CTGTGACCTCTCTGCTCTTCAACATCTGCTCATCACTAGACCTGACCTTCCTGCTGGCT	698	
QY	117	SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet	136	
DB	699	ACCGAGGGGTCTCATACCGGAGCCACAGAGGATGACACGGCGGAGTGGCAAGATG	758	
QY	137	ValAlaValITrPILeLeuAlaPheLeuValAsnGlyPrometIleLeuAlaSerAspSer	156	
DB	759	CTGCTGAGTGGGTGCTGCTGCTTCCTGCTGACGAGCAGCCATCTCTG-----AGC	809	
QY	157	TrpLys-----AsnSerThrAsnThrLysAspCysGlnProGlyPheVal	171	
DB	810	TGGAGATCACTGTCCGGGGGACAGCTCCATCCCCAGGGCCACTGTATAGCCGAGTTCTTC	869	
QY	172	ThrGlnTyrIleLeuThrIleThrMetLeuLeuGlnPheLeuLeuProValIleSer	191	
DB	870	TACAACCTGATCTTCTCATCAGCGCTTCCACCTCGAGATTCTTAAACCCCTTCTCAAGC	929	
QY	192	ValAlaTyrPheAsnValGlnIleTyr-----	200	
DB	930	GTCACCTTCTTAACTCAGATCTTACTGAAATCCAGAGCGACCCGCTCCGGCTG	989	
QY	200	-----	200	
DB	990	GATGGGGCTCGAGAGGACGCGGCCGACGCCCTCCCGAGGCCACCCCTCAACACACC	1049	
QY	201	-----TrpSerLeuTyrLysArgAlaLeuSerArgCysProSerHis	215	
DB	1050	CCACGCGCTGCTGCTGGGCTGCTGAGAGAGGGGACGCGGAGCCATCGCTGCTGAC	1109	
QY	216	-----AlaGlyPheSerThrThrSerSer	223	
DB	1110	AGGTATGGGTGGGTGAGCGGCGCGCTGAGCGCGGAGAGCGAACCTTCGGGGGT	1169	
QY	224	SerAlaSerGlyHisLeuHisArgAlaGlyAlaCysArgThrSerAsnProGlyLeu	243	
DB	1170	GGCGGTGGGGG-----GGCTCGGTGGTTACCACTCACTCAAGCTCGGGC---	121	
QY	244	LysGlnSerAlaValaSerArgHisSerGlnSerProArgArgLysSerSerIleLeuVal	263	
DB	1215	-----ACCTCTCGAGGGGCACTAGAGCGCGGC-----	1244	
QY	264	SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheThrArg	283	

Db 1245 -----TCACTCAAGAGGGCTCCAAAGCGTCG 1271
 QY 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294
 Db 1272 GCGTCCTCGGCTCCTCACTGGAGAGCGCATGAAGTGTGCCAAGCTTCACCCAGCGC 1331
 QY 295 AlaGluLeuLeuArgGlyArgGlyLeuAlaArgSerLeuAlaLeuLeuSerAlaPhe 314
 Db 1332 TTTCGGCTGTCTCGGAGCAAGAAAGTGCCCAAGTCGTGGCCGTCATCGTAGCATCTTT 1391
 QY 315 AlaIleCysThrAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProAlaGlyThr 334
 Db 1392 GGGCTGTGGGGCCCAATACAGCTGTGTATGATCATCCGGCCGCTGCCATGGCCAC 1451
 QY 335 GluArgProLeuSerValTyrTyrSerIleAlaPheTyrLeuGlnTyrPheAsnSerPhe 354
 Db 1452 TGGGTGCTCT--GACTACTGTATGAAACCTCTTCGTGGCTCTGTGGGCCAATCGGCT 1508
 QY 355 ValAsnProPheLeuTyrProLeuCysValArgArgPheGlnIleValAlaPheTyrIle 374
 Db 1509 GTCAACCTGTCTCTCACTGTGTGTGCAACAGCTTCGCGGGGCTTCACCAAGCTG 1568
 QY 375 LeuCysValThrTyr-----ProAlaLeuSerGlnAsnGlnSer 380
 Db 1569 CTCTGCCCCCAGAGCTCAAAATCCAGCCCCCAGACTCTCTGAGCACTGTGAAAGTGA 1628
 QY 381 -----ProAlaLeuSerGlnAsnGlnSer 388
 Db 1629 GTGGCCCAAGAGCTCTCTCAAGCCAGCGCTCTCTCAAGCCAGGTT 1676

RESULT 5
 US-09-165-543-1
 ; Sequence 1, Application US/09165543
 ; Patent No. 6093545

GENERAL INFORMATION:

APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman
 TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHYTE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/165,543

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/042,780

FILING DATE:

ATTORNEY/AGENT INFORMATION:
 NAME: Elizabeth A. Hanley
 REGISTRATION NUMBER: 33,505
 REFERENCE/DOCKET NUMBER: MNI-032CP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 2689 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS

LOCATION: 291..1625
 US-09-165-543-1

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
4,876-65	724.50	48.90%	37.50%	35.38%	3
Length:	2689	Matches:	52	Indels:	12
	171	Mismatches:	118	Gaps:	12

US-10-626-445-8 (1-391) x US-09-165-543-1 (1-2689)

QY 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIle 37
 Db 399 CTGGCCGCGCTCATGGCGGCTGTCTCATCGTGGCCAGCGTGTGGCAACGCGGTGCATG 458
 QY 38 LeuAlaPheValAlaAspArgAsnLeuAlaGlnArgSerAsnTyrPhePheLeuAsnLeu 57
 Db 459 CTGCGCTTCGTGGCCGATCGAGCTTCGAGCCGACCAACAACTTCTTCTGTCAACCTC 518
 QY 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProIleValLeu 77
 Db 519 GCCATCTCCGACTTCTCTGTCGCGGCTTGTGATCTCCATGTATGATACCTACGTGCTG 578
 QY 78 Phe---AsnTyrAsnPheGlySerGlyIleCysMetPheTyrPheLeuIleThrAspTyrLeu 96
 Db 579 ACAGCGCGCTGAGCTTCGCGCGGCGCTGTGCAAGCTGTGCTGAGTGAAGTACACTG 638
 QY 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
 Db 639 CTGTGACCTCCCTCTCTCTCAATCGTGTCTCATGAGTCAACACCGCTTCGTGCTG 698
 QY 117 SerAsnAlaValSerTyrArgAlaGlnIleSerThrGlyIleMetValIleAlaGlnMet 136
 Db 699 ACCGAGCGGTCTCATACGAGGCCAGAGGTGACACGCGGCGGAGTCCGGAAGATG 758
 QY 137 ValAlaValTyrIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
 Db 759 CTGCTGTGTGGTGTGGCTTCTCTGTGTGACGACAGCATCTCG-----AGC 809
 QY 157 TrpIys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
 Db 810 TGGAGTACTGTCTCCGCGGAGCTCATCCCGAGGCGCACCTGATGCGGATCTTCT 869
 QY 172 ThrGluTyrTyrIleLeuThrIleThrMetLeuLeuGluPheLeuProValIleSer 191
 Db 870 TACACTGTACTTCTCTCATACGCGCTTCCACCTGAGTCTTTACGCCCTTCTCAGC 929
 QY 192 ValAlaTyrPheAsnValGlnIleTyr----- 200
 Db 930 GTCACTCTTTTAACTCAGCATCTACCTGAACATCCAGAGGCGCACCGCTCCGGCTG 989
 QY 200 ----- 200
 Db 990 GATGGGCTCGAGAGGAGCGCGCCAGCCCTCTCCGAGGCCACCCCTCAGCACCC 1049
 QY 201 -----TrpSerLeuTyrPlyAspArgAlaLeuSerArgCysProSerHis 215
 Db 1050 CCACGCGCTGTGCTGTGGCGTGTGCGAGAGGCGACGCGGAGGCCATGCGCTGCAC 1109
 QY 216 -----AlaGlyPheSerThrThrSerSer 223
 Db 1110 AGGTATGGGTGGGTAGAGCGCGCTAGAGCGCTGAGGCGCGGAGGAGGACCTCGGGGT 1169
 QY 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
 Db 1170 GCGCGTGGGGG-----GGCTCGGTGCTTCAACCCACCTCCAGCTCGGCG--- 1214
 QY 244 LysGluSerAlaAlaSerArgHisSerGlnSerProArgArgLysSerSerIleLeuVal 253
 Db 1215 -----AGTCTCTGAGGGGCGACTGAGAGGCGCGC----- 1244

QY 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheIleValGlySerPheTrpArg 283
DB 1245 -----TCACTCAAGAGGGGCTCCAAAGCCGTG 1271
QY 284 SerGluSerAlaIleuArgGlnArg-----GluTyr 294
DB 1272 GGGTCTCGGCTCCTGAGAGAAAGCCAGAGATGCTGCCAGAGCTTCACCCAGCGC 1331
QY 295 AlaGluLeuArgGlyArgIleuAlaArgSerIleuAlaIleuLeuSerAlaPhe 314
DB 1332 TTTCGGCTGTCTCGGAGCAAGAAAGTGGCCAAGTCCGTGGCGCTCATCGAGCATCTT 1391
QY 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
DB 1392 GGGCTCTGTGGGCCCCCATACAGCTGTGATGATATATCCGGCCGCTCCAGTGGCCAC 1451
QY 335 GluArgProIysSerValTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPhe 354
DB 1452 TGGCTCCCT---GACTACTGGTACGAAACCTCTTGGCTCTGTGGGCGCACTCGCT 1508
QY 355 ValAsnProPheLeuTyrProIeuCysHisArgArgPheGlnIleValPheTrpIle 374
DB 1509 GTCAACCTGTCTCTACCTGACCTGTGTGCCACACAGCTTCGGCGGCTTCACCAAGCTG 1568
QY 375 LeuCysValThrIle-----Trp-----380
DB 1569 CTCTGCCCCCAAGAAAGCTCAAAATCCAGCCCAAGCTCCCTGGAGCAGCTGTGAGTGA 1628
QY 381 -----ProAlaIeuSerGlnAsnGlnSer 388
DB 1629 GTGGCCCAACAGAGCTCCCTCAGCCAGCCCTCTCTCAGCCCAAGGCT 1676
RESULT 6
US-09-167-354-5
; Sequence 5, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Eklander, Mark
; APPLICANT: Pyatt, Jayashree
; APPLICANT: Huvaf, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
; US-09-167-354-5
Alignment Scores:
Pred. No.: 4,9e-65 Length: 2699
Score: 724.50 Matches: 171
Percent Similarity: 48.908 Conservative: 52
Best Local Similarity: 37.508 Mismatches: 118
Query Match: 35,384 Indels: 115
DB: 3 Gaps: 12
US-10-626-445-8 (1-391) x US-09-167-354-5 (1-2699)
QY 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValAlaIle 37
DB 407 CTGGCCGCGCTCATGCTGCTCATCTGTCGACACGCTGTGGCAACGCGCTGTCATG 466
QY 38 LeuAlaPheValValAsnArgAsnLeuAlaGHisArgSerAsnTyrPhePheLeuAsnLeu 57
DB 467 CTTCGCTTGTGTGGCGCATCTGAGCTTCGCGCACCAAGAACACTTCTTCTGTCTCAACCTTC 526

QY 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77
DB 527 GCCATCTCCGACTTCTCTGTCGGCCCTTTCGATCATCCACATGATGATACCTTACCTGCTG 586
QY 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
DB 587 ACAGGCGCGTGAACCTTGCGCGGGGCTCTGCAAGCTGTGGCTGTGTGGATGAGTACCTG 646
QY 97 LeuCythrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
DB 647 CTGTCACTCTCTCTGCTTCAACATCGTGCTCATCAGTACAGACCGCTTCCTGTGGT 706
QY 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLeuIleValaGlnMet 136
DB 707 ACCCAAGCGGTCTCATACCGGGCCAGAGGGGTGACACGCGCGGCGAGTGGGAGAGT 766
QY 137 ValAlaValAlaIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
DB 767 CTGTGTGTGGTGTGCTGACCTCTGCTGTACGAGACCAACCATCTG-----AGC 817
QY 157 TrpIle-----AsnSerThrAsnThrIleAspCysGluProGlyPheVal 171
DB 818 TGGAGTACCTGTCCGGGGGAGCTCATCCCGAGGGCCACTGTATGCGAGTTC 877
QY 172 ThrGluTrpTyrIleLeuThrIleThrMetLeuGlnPheLeuProValIleSer 191
DB 878 TACAAGTGTACTTCTCTATCAGCGCTTCACCTGTGAGTCTTTCACCCCTTCTCTCAGC 937
QY 192 ValAlaTyrPheAsnValGlnIleTyr-----200
DB 938 GTCACTTCTTTAACCTCAGCATTACTTAATCAATCCAGAGGCGACCCGCTCGGCTG 997
QY 200 -----200
DB 998 GATGGGCTCGAGAGGACCGGCCCCAGACCCCTCCAGAGCCCAAGCCCTCACCAACC 1057
QY 201 -----TrpSerLeuTrpIleArgAlaIleuSerArgCysProSerHis 215
DB 1058 CCACCGCTGTGCTGTGGGCTGTGTGCAGAAAGGGGCAAGGGGAGCCATGCGCTGCAC 1117
QY 216 -----AlaGlyPheSerThrThrsSer 223
DB 1118 AGTATGGGGTGGTGAAGCGGCGCTAGGCGCTGAGCGGGAGAGCCCTCGGGGCT 1177
QY 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
DB 1178 GGGCGTGGGGC-----GGTCCGTGGCTTACCCACTCAGCTCGGCG---1222
QY 244 LysGluSerAlaIleSerArgHisSerGlnSerProArgArgLysSerSerIleLeuVal 263
DB 1223 -----AGTCTCTGAGGGGCACTGAGAGGCGCGC-----1252
QY 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheIleValGlySerPheTrpArg 283
DB 1253 -----TCACTCAAGAGGGGCTCCAGAGCCGTG 1279
QY 284 SerGluSerAlaIleuArgGlnArg-----GluTyr 294
DB 1280 GGGTCTCGGCTCCTGGAAGAGGCAATGAAGTGTCTCCAGAGCTTCACCCAGAGC 1339
QY 295 AlaGluLeuArgGlyArgIleuAlaArgSerIleuAlaIleuLeuSerAlaPhe 314
DB 1340 TTTCGGCTGTCTCGGAGCAAGAAAGTGGCAAGTGTGCGCGTGCATGTGAGCATCTT 1399
QY 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
DB 1400 GGGCTCTGTGGGCCCCATACAGCTGTGATGATATATCCGGCCGCTTCAGTGGCCAC 1459
QY 335 GluArgProIysSerValTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPhe 354
DB 1460 TGGCTCCCT---GACTACTGGTACGAAACCTCTCTGTGGCGCAACTCGGCT 1516

QY 355 ValAsnProPheLeuTyProLeuCyHisArgArgPheGlnIleValaPheTPrIle 374
DB 1517 GTGACCTGTGTCTTACCTCTGTGTGCACACAGCTTCGGCGGGCTTACCAAGCTG 1576
QY 375 LeuCyValThrIle-----TTP----- 380
DB 1577 CTGTGCCCCCAAGAGCTCAAAATCCAGCCCCACAGCTCCCTGAGACCTGTGAAAGTGA 1636
QY 381 -----ProAlaLeuSerGlnAsnGlnSer 388
DB 1637 GTGGCCCAACAGAGCTCCCTCAGCCACAGCTCTCTCAGCCCAAGTCT 1684

RESULT 7
US-09-642-855-5
Sequence 5, Application US/09642855
Patent No. 643743
GENERAL INFORMATION:
APPLICANT: Lovenberg, Timothy
APPLICANT: Briander, Mark
APPLICANT: Pyatt, Jayashree
APPLICANT: Huvar, Arne
TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
TITLE OF INVENTION: SUBTYPE
FILE REFERENCE: JMW
CURRENT APPLICATION NUMBER: US/09/642,855
CURRENT FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: 09/167,354
PRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 2699
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-855-5

Alignment Scores:
Pred. No.: 4,9e-65 Length: 2699
Score: 724.50 Match: 171
Percent Similarity: 48.90% Conservative: 52
Best Local Similarity: 37.50% Mismatches: 118
Query Match: 35.38% Indels: 115
Gaps: 12

US-10-626-445-8 (1-391) x US-09-642-855-5 (1-2699)

QY 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIle 37
DB 407 CTGGCGCGGCTCATGGCGGTGCATCGGCCAGCGGTGCGGCAACGGCGTGTCTATG 466
QY 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrrPhePheLeuAsnLeu 57
DB 467 CTGCGCTTGTGGCCACCTCGAGCTCCGACCCCAACAACACTTCTTCCGCTCAACCTC 526
QY 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrrIleProHisValLeu 77
DB 527 GCCATCTCCGACTTCTCTCGTGGCGGCTTCTGCATCCCATGTATGTACCTTACGTCG 586
QY 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrrLeu 96
DB 587 ACAGGCGGCTGACCTTGGCGCGGGGCTGTGCAACGTGCTGTGATGAGACTACCTG 646
QY 97 LeuCyThrAlaSerValTyrrAsnIleValLeuIleSerTyrrAspArgTyrrGlnSerVal 116
DB 647 CTGTGACCTCTCTGCTTCAACATCGTCTCATCAGCTACCAACGCTTCTGTGAGTC 706
QY 117 SerAsnAlaValSerTyrrArgAlaGlnHisThrGlyIleMetTyrrIleValAlaGlnMet 136
DB 707 ACCCGAGCGGTCTCATACCGGCGCCAGCGAGTGACACCGCGGCGGAGTGGCGGAAGATG 766
QY 137 ValAlaValAlaTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156

DB 767 CTGCTGTGTGGGTGCTGGCTCTTCTGTGTACGAGACCAAGCCATCCTG-----AGC 817
QY 157 TrpIle-----AsnSerThrAsnThrIleValAspArgGlnProGlyPheVal 171
DB 818 TGGAGATACCTGTCCGGGGGACGCTCATCCCGAGGGCCACATGTATGCGAGTCTTC 877
QY 172 ThrGlyTrpTyrrIleLeuThrIleThrMetLeuGlnPheLeuProValIleSer 191
DB 878 TACAACCTGTACTTCTCATACAGGCTTCCACCCCTGGAGTCTTTACGCCCTTCTCAGC 937
QY 192 ValAlaTyrrPheAsnValGlnIleTyrr----- 200
DB 938 GTCACTCTTTTAACTCAGACATCTTACCTGAACATCCAGAGGCCACCGCTCCGGCTG 997
QY 200 ----- 200
DB 998 GATGGGCTCGAGAGGACCGGCCCCGAGCCCCCTCCGAGGCCAGCCCTCACCAACC 1057
QY 201 -----TrpSerLeuTrpIleAspArgAlaLeuSerArgCysProSerHis 215
DB 1058 CCAGCCCTGTGCTGTGGGGCTGTGTGCAAGAGGGCAGGGAGGCCATGCCGTGCAC 1117
QY 216 -----AlaGlyPheSerThrThrSerSer 223
DB 1118 AGGTATGGGTGGGTGAGGCGGCCGCTGAGCGCTGAGCGGGAGGCGACCTCGGGGCT 1177
QY 224 SerAlaSerGlyHisIleuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
DB 1178 GCGGTGGGGGCT-----GGCTCGGTGCTTCAACCACTTCAGCTCCGCTC 1222
QY 244 LysGluSerAlaAlaSerArgHisSerGlnSerProArgArgLysSerSerIleLeuVal 263
DB 1223 -----AGCTCTCGAGGGGCACTGAGAGCCGCGC----- 1252
QY 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheValGlySerPheTyrrArg 283
DB 1253 -----TCACTCAAGAGGGGCTCAAGCCGCTG 1279
QY 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyrr 294
DB 1280 GCGCTCTGCTGGGCCCATACAGCGCTGATGATCATCCGGGCGGCTGCATGGCCAC 1459
QY 295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
DB 1340 TTTCGGCTGTCTGGACAGGAAGTGGCCAACTGCTGCGCTGCTGAGCACTTT 1399
QY 315 AlaIleCyrrTrpAlaProTyrrCysLeuPheThrIleValLeuSerThrTyrrProArgThr 334
DB 1400 GGGCTCTGCTGGGCCCATACAGCGCTGATGATCATCCGGGCGGCTGCATGGCCAC 1459
QY 335 GluArgProLysSerValTrpTyrrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPhe 354
DB 1460 TGGGTGCTCT---GACTACGTGATACGAACCTCTTGTGCTCTGTGGGCAACTGGCT 1516
QY 355 ValAsnProPheLeuTyrrProLeuCyHisArgArgPheGlnIleValaPheTPrIle 374
DB 1517 GTCAACCTGTCTCTTACCTCTGTGTGCACACAGCTTCGGCGGGCTTACCAAGCTG 1576
QY 375 LeuCyValThrIle-----TTP----- 380
DB 1577 CTGTGCCCCCAAGAGCTCAAAATCCAGCCCCACAGCTCCCTGAGACCTGTGAAAGTGA 1636
QY 381 -----ProAlaLeuSerGlnAsnGlnSer 388
DB 1637 GTGGCCCAACAGAGCTCCCTCAGCCACAGCTCTCTCAGCCCAAGTCT 1684

RESULT 8
US-09-642-514-5
Sequence 5, Application US/09642514
Patent No. 6437100
GENERAL INFORMATION:
APPLICANT: Lovenberg, Timothy

Query Match: 35.284 Indels: 93
DB: 3 Gaps: 10

US-10-626-445-8 (1-391) x US-09-167-354-6 (1-1335)

QY 18 LeuAlaPheLeuMeSerSerPheAlaPheAlaIleMeValGlyAsnAlaValIle 37
DB 109 CTGGCCGCGCTCATGGCGCTCATGTCGGCCAGCCGCTGGCGCAACCGCGTGGT CATG 168

QY 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnIlePhePheLeuAsnLeu 57
DB 169 CTGGCTTGTGGCCGCACTGCGACCTCCGACCCAGAACAACTTCTTCCTGCTCAACCTC 228

QY 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrlleProHisValLeu 77
DB 229 GCCATCTCCGACTTCTCTCGCGCGGCTTCGTGATCCCACTGATGATGACCTTACGTCG 288

QY 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrlleu 96
DB 289 ACAGCGCGCTGGACCTTCCGCGCGGCTCTGCAAGCTGTGCTGGTAGTGACTACCTG 348

QY 97 LeuCyThrAlaSerValTyrlAsnIleValIleIleSerTyrlAspArgTyrlGlnSerVal 116
DB 349 CTGTGCACTCTCTGCTGCTCAACATGTGCTCATAGCTACGACCGCTTCTGTGCGTCT 408

QY 117 SerAsnAlaValSerTyrlArgAlaGlnHisThrGlyIleMetValIleValIleGlnMet 136
DB 409 ACCCGAGCGGCTTCACACCGCGGCCAGCAGGAGACCGCGGGGCGGACGTGCGGAAGATG 468

QY 137 ValAlaValTyrlleuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
DB 469 CTGCTGTGTGGGTGCTGGCTCTCTGCTGTACGACACGACCATCTCGT-----AGC 519

QY 157 TrpLys-----AsnSerThrAsnThrIleLysAspArgGlnProGlyPheVal 171
DB 520 TGGAGTACCTGTCCGAGGCGACGCTCATCCCGAGGCGCACGTGATGCCAGTCTTTC 579

QY 172 ThrGlnTrpTyrlleuLeuThrIleThrMetLeuGlnPheLeuLeuProValIleSer 191
DB 580 TACAATGATGATCTCTCATACACGCTTCCACCGTGAAGTCTTTACGCCCTTCTCCACG 639

QY 192 ValAlaTyrlPheAsnValGlnIleTyrl----- 200
DB 640 GTACACCTCTTTAACTCTCAGCATCTACTGACATCCAGAGCGCACCCGCTCCGAGT 699

QY 200 ----- 200

DB 700 GATGGGCTCGAGAGCGCGGCCGCCGAGCCCTCCGAGGCCAGCCCTTCAACACCC 759

QY 201 ----- 215
DB 760 CCAACCGCTGCTGCTGGGCTGCTGCGCAAGAGGCGACGCGGACCATGCGCTGCAC 819

QY 216 ----- 223
DB 820 AGGATAGGGGTGGGTGAGCGCGCGCTAGCGCTGAGCGCGGAGAGCGCCCTCGGGGT 879

QY 224 SerAlaSerGlyHisIleuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
DB 880 GCGCGTGGGGC-----GGCTCCGTGGCTTCAACCCACCTCCAGCTCCGCGC--- 924

QY 244 LysGlnSerAlaAlaSerArgHisSerGlnSerProArgArgLysSerSerIleLeuVal 263
DB 925 -----AGCTCCCTCGAGGCGGACATGAGAGCCCGC----- 954

QY 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheIleValGlySerPheTyrlleu 283
DB 955 -----TCACTCAAGAGGCGGCTTCAAGCGCTCG 981

QY 284 SerGlnSerAlaAlaLeuArgGlnArg-----GluTyrl 294
DB 982 GCGTCTCGGCTCGCTCGAGAGCGCATGAGATGATGTGTCCAGAGCTTCAACCGAGCCG 1041

QY 295 AlaGlnLeuLeuArgGlyArgIleValArgSerLeuAlaIleLeuLeuSerAlaPhe 314
DB 1042 TTTCGGCTGTCTCGGAGAGAGAGAGGCGCAAGTGGTGGCGGTCACTGAGCATCTT 1101

QY 315 AlaIleCysTrpAlaProTyrlCysLeuPheThrIleValLeuSerThrTyrlProArgThr 334
DB 1102 GGGCTCTGTGGGCGCCCAACACGCTGATGATATATCGGGCGCGCTGCCATGGCCAC 1161

QY 335 GluArgProLysSerValTyrlTyrlSerIleAlaPheTrpLeuGlnTrpPheAsnSerPhe 354
DB 1162 TGGCTCCCT---GACTAGTGATGCAAACTCTTGTGCTCTGCGGCAACTGGCT 1218

QY 355 ValAsnProPheLeuTyrlProLeuCysHisArgArgPheGlnValAlaPheTrpValIle 374
DB 1219 GTCAACCTGTGCTCTTACCTCTGTGCGCACACAGCTTCCGCGGCGCTTCAACAGCTG 1278

QY 375 LeuCyValAlThrLys 379
DB 1279 CTCTGCCCCAGAGG 1293

RESULT 12
US-09-642-855-6
Sequence 6, Application US/09642855
Patent No. 6413743
GENERAL INFORMATION:
APPLICANT: Lovenberg, Timothy
APPLICANT: Brlander, Mark
APPLICANT: Pyati, Jayashree
APPLICANT: Hovav, Arne
TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
FILE REFERENCE: JMW
CURRENT APPLICATION NUMBER: US/09/642,855
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/167,354
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 1335
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: cDNA
US-09-642-855-6

Alignment Scores:
Pred. No.: 2.5e-65 Length: 1335
Score: 722.50 Matches: 165
Percent Similarity: 50.82% Conservative: 51
Best Local Similarity: 38.82% Mismatches: 116
Query Match: 35.284 Indels: 93
DB: 3 Gaps: 10

US-10-626-445-8 (1-391) x US-09-642-855-6 (1-1335)

QY 18 LeuAlaPheLeuMeSerSerPheAlaPheAlaIleMeValGlyAsnAlaValIle 37
DB 109 CTGGCCGCGCTCATGGCGCTCATGTCGGCCAGCCGCTGGCGCAACCGCGTGGT CATG 168

QY 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnIlePhePheLeuAsnLeu 57
DB 169 CTGGCTTGTGGCCGCACTGCGACCTCCGACCCAGAACAACTTCTTCCTGCTCAACCTC 228

QY 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrlleProHisValLeu 77
DB 229 GCCATCTCCGACTTCTCTCGCGCGGCTTCGTGATCCCACTGATGATGACCTTACGTCG 288

QY 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrlleu 96
DB 289 ACAGCGCGCTGGACCTTCCGCGCGGCTCTGCAAGCTGTGCTGGTAGTGACTACCTG 348

QY 97 LeuCyThrAlaSerValTyrlAsnIleValIleIleSerTyrlAspArgTyrlGlnSerVal 116

Db	349	CTGTGCACTCTCTCTGCTTCAACATCGTGCCTCATCACTAGACACCGCTCTCTCGGATC	408
Qy	117	SerSanaIaValSerTyrArgIaGlnIhIsthrGlyIleMetLysIleValAlaGlnMet	136
Db	409	ACCCGAGGCGCTCTCATACCGGGCCAGAGGGTGAACGCGGCGGGCAGTGGAGAAATG	468
Qy	137	ValaIaValTrrIleLeuAlaPheLeuValAasnGlyProMetIleLeuAlaSerAspSer	156
Db	469	CTGCTGCTGTGGGTCTGACCTCTTCTGCTGTACGAGCAACGCAATCTCTG-----AGC	519
Qy	157	TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal	171
Db	520	TGGGAGTACTGTCCGGGGGAGCTCCATCCCGAGGGCCACTGCTATAGCCAGATTCTTC	579
Qy	172	ThrgIuTrrPrrIleLeuThrIleThrmethLeuGluPheLeuLeuProValIleSer	191
Db	580	TACAACGTGTACTTCTCATCAAGGCTTCACCTTGAGTGTCTTAACGCTCTTCTCAAGC	639
Qy	192	ValaIaTrrPheAsnValGlnIleTyr-----	200
Db	640	GTCACCTTCTTTAACTCAGACATCAACCTGAACATCAAGAGCGACCGCGCTCCGGGTG	699
Qy	200	-----	200
Db	700	GATGGGCTCGAGAGCAGCGGCCCCGAGCCCCCTCCGAGGCCAAGCCCTACCAACC	759
Qy	201	-----TrpSerLeuThrTrpAspArgIaIaLeuSerArgCysProSerHis	215
Db	760	CCACCGCTGGCTGCTGGGGCGTCTGGAGAAAGGGGCACAGGGAGAGCCATGCCCTGCAC	819
Qy	216	-----AlaGlyPheSerThrThrSerSer	223
Db	820	AGTATGGGATGGGTGAAGCGGCCCTGAGCGCTGAGCGCGGGAGAGCCACTCCGAGGGT	879
Qy	224	SerIaSerGlyHisIleuHisIaArgIaGlyValaIaCysArgTrpSerAsnProGlyLeu	243
Db	880	GCGCGTGGGGC-----GGCTCCGGGGCTTACCAACCATCTTCAAGCTCCGGC---	924
Qy	244	LysGluSerAlaIaIaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal	263
Db	925	-----ACCTCTTCAGGGGGCATGAGAGCGCGCC-----	954
Qy	264	SerLeuArgThrHisMetLysSerSerIleThrIaPheLysValGlySerPheTrpArg	283
Db	955	-----TCATCAAGAGGGGCTCCAAAGCCGTGC	981
Qy	284	SerGluSerAlaIaIaLeuArgGlnArg-----GluTyr	294
Db	982	GCGTCTCTGGCTCGCTCGTAGAGAGGCATGAAGATGTGTCCCAAGCTTACCAACGAGGC	1044
Qy	295	AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe	314
Db	1042	TTTGGCTGTCTCGGGAGAGAAAGTGGCCAAAGTGGTGGCCGTATGGTGGACATCTTT	1101
Qy	315	AlaIleCysTrrPrrAlaProTrrCysLeuPheThrIleValIleuSerThrTyrProArgThr	334
Db	1102	GGGCTCTCTGGGCCCCCATACCGCTGCTGATGAATCATTCGGGCGCGCTCCATGGCCAC	1161
Qy	335	GluArgProLysSerValTrrPrrSerIleAlaPheTrpLeuGlnTrrPheAsnSerPhe	354
Db	1162	TGCGTCCCT---GACTACTGGTGAACAAACCTCTTCTGTGGCTCTGTGGGCAACTCGGCT	1218
Qy	355	ValAsnProPheLeuTrrProLeuCysHisArgArgPheGlnLysAlaPheTrrPrrLysIle	374
Db	1219	GTCAAACCTGTCTTACCTCTGTGGCACAACAAGCTTCGCGGGGCTTCAACCAAGCTG	1278
Qy	375	LeuCysValThrLys	379
Db	1279	CTCTGCCCCCAGAAAG	1293

DB	Seq	Accession	Length	Score	Similarity	Local Similarity	Match	Mismatch	Indel	Gap
US-10-626-445-8	(1-391) x US-09-642-514-6	(1-1335)								
DB	18	LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValIGlyAsnAlaValIle	1335	2.5e-65	722.50	50.824	165	51	116	93
DB	109	CTGGCCGCGCTATGCGCGCTGCTCATCGCGCCAGCGCTGGGCAACGCGCTGCTATG	166			35.284				10
DB	38	LeuAlaPheValValaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu	57							
DB	169	CTGGCCTTGGTGGCCGACCTGACGCTCGGACCCGAAACATCTTCTGCTCAACCTC	228							
DB	58	AlaIleSerAspPheLeuValIGlyLeuIleSerIleProLeuTyrIleProHisValLeu	77							
DB	229	GCCATCTCGACTTCTGCTGCGCGCCCTTGTGCATCCACATGATGACCTTACCTGCTG	288							
DB	78	Phe---AsnTyrAsnAspPheGlySerGlyIleCysMetPheTyrPheLeuAspTyrLeu	96							
DB	289	ACAAGCGCGCTGACCTTGGCGCGGGGCTGTGCAAGCTGTGGCTGATGATGACTTACCTG	348							
DB	97	LeuCyethAlaSerValTyrAsnIleValIleIleSerTyrAspArgTyrGlnSerVal	116							
DB	349	CTGTGACCTCTCTGCTGCTCAACATCGTGTGCATCACTACAGACCGCTTCTGTGCTG	408							
DB	117	SerAsnAlaValSerTyrArgIleGlnHisIleThrGlyIleMetCysIleAlaGlnMet	136							
DB	409	ACCGAGCGGCTCTCAACCGGGCCAGCAGGATGACACGGCGGGGAGAGTGGGAGATG	468							
DB	137	ValAlaValTyrPheLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer	156							
DB	469	CTCTGTGTGTGGTGTGGCTTCTTCTGCTGACGAGACGACGATCTCG-----AGC	519							
DB	157	TyrPhe-----AsnSerThrAsnThrLysAspCysGlnProGlyPheVal	171							
DB	520	TGGGAGAACCTGTCCGGGGGAGCTCAATCCCGAGGGCCACTGTATGCCGATTTTC	579							
DB	172	ThrGluTyrTyrIleLeuThrIleThrMetLeuLeuGlnPheLeuAsnProValIleSer	191							
DB	580	TACACCTGGATCTCTCATCAACGGCTTCAACCGTGAATCTTAAAGCCCTTCTCAGC	639							
DB	192	ValAlaTyrPheAsnValGlnIleTyr-----	200							
DB	640	GTCACCTCTTAACTTCACTGATCTTCACTGAACATCAGAGCGCACCGCTCCGCTG	699							

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QY 200 ----- 200
Db 700 GATGGGGCTGAGAGGAGCGGCGCCGAGCCCTCCGAGGCCAGCCCTCAACACC 759
QY 201 -----TTPSerLeuThrLysArgArgAlaLeuSerArgCysProSerHis 215
Db 760 CCACCGCTGGCTGCTGGGCTGCTGGCAGAGGGGAGCGGAGCCATGCGCTGCAC 819
QY 216 -----AlaGlyPheSerThrThrSerSer 223
Db 820 AGGTATGGGTGGGTGAGCGCGCCGTAAGCCCTGAGGCGGAGGAGCCCTTCGGGGGT 879
QY 224 SerAlaSerGlyHisLeuHisArgAlaGlyAlaCysArgThrSerAsnProGlyLeu 243
Db 880 GCGGTGGGGGCG-----GGCTCGGTGCTTCAACCCACTCCACTCCGGC--- 924
QY 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal 263
Db 925 -----AGCTCTCGAGCGGCACTGAGAGCGCGCGC----- 954
QY 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheThrArg 283
Db 955 -----TCACTCAAGAGGGGCTCCAGCCGCTCG 981
QY 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294
Db 982 GCGTCTCGGCTCGCTCGGAGAGCGCATGAGTGTCCAGAGCTTCACCCAGCGC 1041
QY 295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
Db 1042 TTTCGGCTGTCTCGGGAGAGAAAGTGGCCAAAGTCCGCTGCGCTCATCGAGCATCTTT 1101
QY 315 AlaIleCysThrAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db 1102 GGGCTGTGCTGGGCGCCCATACAGCTGCTGATATCATCCGGCGCGCTCCATGGCCAC 1161
QY 335 GluArgProLysSerValTTPYrSerIleAlaPheThrLeuGlnThrPheAsnSerPhe 354
Db 1162 TGGGTCCT---GACTACTGTGATCGAAACTCTTCCTGCTGCTCGTGGCCACTCGGCT 1218
QY 355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheThrLysIle 374
Db 1219 GTCAACCTGTCTCTTCACTCTGTGCAACAGCTTCGCGCGGCTTCACCAAGCTG 1278
QY 375 LeuCysValThrLys 379
Db 1279 CTCTGCCCCCAGAG 1293

RESULT 14
US-09-891-053-21
Sequence 21. Application US/09891053
GENERAL INFORMATION:
APPLICANT: Icadani, Hiraiku
APPLICANT: Takimura, Tetsuo
APPLICANT: Nakamura, Takao
APPLICANT: Kobayashi, Masahiko
APPLICANT: Tanaka, Ken-ichi
APPLICANT: Hidaka, Yuseuke
TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
FILE REFERENCE: 06501-083001
CURRENT APPLICATION NUMBER: US/09/891,053
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: PCT/JP99/07280
PRIOR FILING DATE: 1999-12-24
PRIOR APPLICATION NUMBER: PCT/JP98/05967
PRIOR FILING DATE: 1998-12-25
PRIOR APPLICATION NUMBER: JP 11/145661
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 26

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SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 2050
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (271)...(1629)
US-09-891-053-21

Alignment Scores:
Pred. No.: 5,05e-65 Length: 2050
Score: 722.50 Matches: 165
Percent Similarity: 50.82% Conservative: 51
Best Local Similarity: 38.82% Mismatches: 116
Query Match: 35,28% Indels: 93
DB: 4 Gaps: 10

US-10-626-445-8 (1-391) x US-09-891-053-21 (1-2050)
QY 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaMetValGlyAsnAlaValIle 37
Db 379 CTGGCGCGCTCATGGCGGCTGCTCATGTGGCCAGCGTGTGGCAACGGCTGTGATG 438
QY 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 439 CTGCGCTTGTGGCGCATCGAGCTCCGACCCAGAACACTTCTTCCTGCTCAACCTC 498
QY 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77
Db 499 GCCATCTCGCACTTCTCGTGGCGCTTCTGTGATCCCACTGATATCTACCTACGTGCTG 558
QY 78 Phe---AsnThrAsnPheGlySerGlyIleCysMetPheThrLeuIleThrAspTyrLeu 96
Db 559 ACAGCGCGCTGACCTTCCGCGGCGCTCTGTGACGTGGTGTGTAGTGAAGTACCTG 618
QY 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 619 CTGTGACCTCCCTCTGCTTCAACATCGTGTATCATAGTACGAGCGCTTCCTGCTGCTG 678
QY 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136
Db 679 ACCCGAGCGGTCTCATACCGGCGCCAGAGGTGACACCGCGGCGGACGTGCGAAGATG 738
QY 137 ValAlaValThrIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 739 CTGCTGTGTGTGTGTGGCTTCTCTGTGTGATCGAGCCAGCCATCTCTG-----AGC 789
QY 157 TTPYrS-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
Db 790 TGGGATACCTCTGCGGGGAGCTCATCCCGAGGGCACTGCTATGCCAGTCTTC 849
QY 172 ThrGluTTPYrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuProValIleSer 191
Db 850 TCAACCTGTACTTCTCTCATACAGGCTTCACCTGTGAGTTCTTACGCCCTTCCTCAGC 909
QY 192 ValAlaTyrPheAsnValGlnIleTyr----- 200
Db 910 GTCACTCTTTAATCTCAAGATCTGAACATCCAGAGGGACCCGCTCGGCTG 969
QY 200 ----- 200
Db 970 GATGGGCTCGAGAGCGAGCCGCGCCGAGCCCTCCGAGGCCAGCCCTCAACACC 1029
QY 201 -----TTPSerLeuThrLysArgArgAlaLeuSerArgCysProSerHis 215
Db 1030 CCACCGCTGTGCTGTGGGCTGCTGGCAGAGGGGAGCGGAGGCCATGCGCTGCAC 1089
QY 216 -----AlaGlyPheSerThrThrSerSer 223
Db 1090 AGGTATGGGTGGGTGAGCGCGCCGTAAGCCCTGAGGCGGAGCGGAGCCCTTCGGGGGT 1149
QY 224 SerAlaSerGlyHisLeuHisArgAlaGlyAlaCysArgThrSerAsnProGlyLeu 243

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Db      1150 GCGCGTGGGGGC-----GGCTCCGTGGCTTCAACCACTCCAGCTCCGCGC--- 1194
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Qy      264 SerLeuArgThrHisMetAnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283
Db      1225 -----TACTCAAGAGGGGCTCCAAAGCGGTGC 1251
Qy      284 SerGUserAlaAlaLeuArgGlnArg-----GluTyr 294
Db      1252 GGGCTCTGGCGCTCGTGGAGAGCGCATGAAGATGTGTCCAGAGCTTCAACCCAGCGCC 1311
Qy      295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuSerAlaPhe 314
Db      1312 TTTCGGCTCTTCGGGACGAGAAAGTGGCCAGTCCGCTGCGTCACTGAGCATCTTT 1371
Qy      315 AlaIleCyStrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
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RESULT 15
US-09-165-543-6
; Sequence 6, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D. J. Goodearl and Sandra Gluckman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNT-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)742-4214
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1338 base pairs
; TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
; US-09-165-543-6

Alignment Scores:
Pred. No.: 1,066-64 Length: 1338
Score: 716.50 Matches: 165
Percent Similarity: 53.41% Conservative: 54
Best Local Similarity: 40.24% Mismatches: 128
Query Match: 34.99% Indels: 63
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Qy      38 LeuAlaPheValAlaAspArgAsnLeuArgHisSerAsnTyrPhePheLeuAsnLeu 57
Db      169 CTGGCTGTGGCGGATTCGAGCTTCGACCCAGAAACACTTCTTCTGCTCAACTC 228
Qy      58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValIleu 77
Db      229 GCATCTCGCATCTCTCTGTGGGTGCTTCGATCCCATGTGATGACCATGCTGCTG 288
Qy      78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
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Qy      97 LeuCyThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db      349 CTGTGTGCTCTCTCGCTCTTCAACTGACTCATCACTGATGACATTCCTGCTCACTG 408
Qy      117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136
Db      409 ACTGAGGTGTCTCTCAAGGGCCAGGAGGAGGACAGAGAGCGGCGCTTCGGAATG 468
Qy      137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db      469 GCACGTGTGTGGTCTGCTGCTGTGATGGGCGTCCGATCTG-----AGT 519
Qy      157 TrpLys-----AsnSerThrAsnThrLysAspCyGluProGlyPheVal 171
Db      520 TGGAGTACTGTCTGTGGGCACTTCATCCCGAGGGCCACTGTATGCTGAGTTCTTC 579
Qy      172 ThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuProValIleSer 191
Db      580 TACAAGTGTACTTCTCATACAGGCGCTCCACCCCTGAGTTCTTACGCCCTTCAAGC 639
Qy      192 ValAlaTyrPheAsnValGlnIleTyrTrpSerLeuTrpLysArgArgAlaLeu----- 209
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Qy      210 -----SerArgCysProSerHis 215
Db      700 GATGGGGGCGGTGAGGCTGGGCCAGAACCCCAACCAATGCCAGCTCGCCACTCTCCA 759
Qy      216 AlaGlyPheSerThrThrSerSerSerAlaSerGlyHis-----LeuHis 230
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Qy      231 ArgAlaGlyValAlaCyAsnArgThrSerAsnProGlyLeuLys----- 244
Db      820 AGGTATGGGGTGGGT-----GAGGCAAGCCCTGTGTGTGAGGCTGGGAGGCTGCCCTC 873
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QY 290 ArgGlnArgGlnTyrAlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIle 309
Db 1033 ACCCAAGCGC-----TTCGGGCTGTTCGGGACACAGAGGTGGCCAACTGCTGGCCATC 1086
QY 310 LeuLeuSerAlaPheAlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSer 329
Db 1087 ATCGTGAGCATCTTTGGGCTCTGCTGGGCGCGGACACGCTCCTAATGATCATCCGAGCT 1146
QY 330 ThrTyrProArgThrGluArgProLysSerValTrpTyrSerIleAlaPheTrpLeuGln 349
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QY 350 TrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLys 369
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Search completed: October 8, 2005, 04:47:20
Job time : 244 secs

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SUMMARIES

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(without alignment)
3091.093 Million cell updates/sec

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Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
delop	6.0	delext	7.0

Searched: 8443130 beqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16886260

Maximum DB seq length: 20000000000

Post-processing:	Minimum Match	0%
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Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bitsmax2
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100
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SUMMARIES

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4	1745	88.2	US-10-626-126-6	Sequence 6, Appl
5	1745	88.2	US-10-626-126-6	Sequence 6, Appl
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7	1370.5	66.9	US-09-812-216-1	Sequence 1, Appl
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9	1370.5	66.9	US-09-812-216-1	Sequence 1, Appl
10	1370.5	66.9	US-09-812-216-1	Sequence 1, Appl
11	1370.5	66.9	US-10-052-193-1	Sequence 1, Appl
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23	1370.5	66.9	US-10-354-769-1	Sequence 1, Appl
24	1370.5	66.9	US-10-354-769-1	Sequence 1, Appl
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26	1370.5	66.9	US-10-354-769-1	Sequence 1, Appl
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28	1370.5	66.9	US-10-354-769-1	Sequence 1, Appl
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33	1370.5	66.9	US-10-354-769-1	Sequence 1, Appl
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37	1370.5	66.9	US-10-354-769-1	Sequence 1, Appl
38	1370.5	66.9	US-10-354-769-1	Sequence 1, Appl
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43	1370.5	66.9	US-10-354-769-1	Sequence 1, Appl
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45	1370.5	66.9	US-10-354-769-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
 US-10-626-445-5
 ; Sequence 5, Application US/10626445
 ; Publication No. US20040248252A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ldu, Changlu
 ; APPLICANT: Lovemberg, Timothy
 ; TITLE OF INVENTION: DnaB Encoding Mammalian Histamine Receptor Of The H4 Subtype
 ; FILE REFERENCE: PRD-0032
 ; CURRENT APPLICATION NUMBER: US/10/626,445
 ; CURRENT FILING DATE: 2003-07-23
 ; PRIOR APPLICATION NUMBER: 09/790,849
 ; PRIOR FILING DATE: 2001-02-22
 ; PRIOR APPLICATION NUMBER: 60/208,260
 ; PRIOR FILING DATE: 2000-05-31
 ; NUMBER OF SEQ ID NOS: 27

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-445-5

Alignment Scores:
Pred. No.:          9,666-215          Length:          1176
Score:             2035.00             Matches:          390
Percent Similarity: 99.74%             Conservative:     0
Best Local Similarity: 99.74%           Mismatches:      1
Query Match:       99.37%              Indels:          0
DB:                20                  Gaps:            0

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QY      21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleleuAlaPhe 40
DB      61 TTAATGCTCTTCAATTCCTTGCTGCTAATAGTGAAGCAATGCTGCTCATTTAGCCTTT 120
QY      41 ValValaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
DB      121 GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCCT 180
QY      61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValleuPheAsnTyr 80
DB      181 GACTTCCTCGTGGGTTTGAATTCATTCCTCTGTATACATCCCTCACAGTGTGTTAACTGG 240
QY      81 AsnPheGlySerGlyIleCysMetPheTyrPheIleThrAspTyrIleuLeuCysThrAla 100
DB      241 AATTTTGGAGAGTGAATTCGATGCTTTTGGCTATTACGACTATCTTTTGGACCCGA 300
QY      101 SerValTyrAsnIleValIleuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
DB      301 TCTGTCTCAAAATATGTCCTCATTAAGTACATCGATCGAATACAGACAGTTCCTCAATGCTGG 360
QY      121 SerTyrArgAlaGlnHisThrGlyIleMetIleValAlaGlnMetValAlaValIleTyr 140
DB      361 TCTTAATAGGCTCAACACACTGGCATCATGAAGATTTGCTCAAAATGAGGCTGTTTGG 420
QY      141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrPheAsnSer 160
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QY      161 ThrAsnThrIleAspCysGluProGlyPheValThrGluTyrIleLeuThrIleThr 180
DB      481 ACGAACACAAAGAGAGCTGAGCTGGCTTTGTTACAGAGGTGATACCTCCACCATTAACA 540
QY      181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
DB      541 ATGCTCTTGAATTCCTGCTTCCTGTCATCTCTGTGGCTTAATTCATGATACGATTTTAC 600
QY      201 TrpSerLeuTyrPheArgAlaIleuSerArgCysProSerHisAlaGlyPheSerThr 220
DB      601 TGGAGCTGTGGAAGGTAGAGGCTCTCAAGTAGGAGCCCTTAGCCATGCTGATTTCTCACT 660
QY      221 ThrSerSerSerAlaSerGlyHisIleuHisArgAlaGlyValAlaCysArgThrSerAsn 240
DB      661 ACTCTTCCAGTGCTTCAGAGACCTTAACACAGAGCTGGGTGGCTTGCAGAGACAACTAAT 720
QY      241 ProGlyLeuLeuGluSerAlaAlaSerArgHisSerGluSerProArgArgIleSerSer 260
DB      721 CCTGGATTTGAAGAATCAGCTGATCTCCGACTCAGAAAGTCCCTCGAAGAAAGACACAG 780
QY      261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLeuValGlySer 280
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QY      281 PheTyrArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGlnIleLeuAlaArgGly 300
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QY      301 ArgIleLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTyrAlaPro 320
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QY      321 TyrCysLeuPheThrIleValleuSerThrTyrProArgThrGluArgProIleSerVal 340
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QY      341 TrpTyrSerIleAlaPheTyrLeuGluTyrPheAsnSerPheValAsnProPheLeuTyr 360
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RESULT 2
US-10-626-126-5
; Sequence 5, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626.126
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-126-5

Alignment Scores:
Pred. No.:          9,666-215          Length:          1176
Score:             2035.00             Matches:          390
Percent Similarity: 99.74%             Conservative:     0
Best Local Similarity: 99.74%           Mismatches:      1
Query Match:       99.37%              Indels:          0
DB:                21                  Gaps:            0

US-10-626-445-8 (1-391) x US-10-626-126-5 (1-1176)

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QY      41 ValValaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
DB      121 GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCCT 180
QY      61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValleuPheAsnTyr 80
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Qy 261 lIleValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheIysValGlySer 280
Db 781 ATCTGGTGTCTCTTAAGACATCCAGACAGACAGATGATCTGCTTCAAAAGGGCTTC 840
Qy 281 PheTPARSerGluSerAlaAlaLeuArgGlnArgGluIleValGluLeuLeuArgGly 300
Db 841 TTCTGGCGATCGGAAAGTCGAGCGCTTCGCCAAGGAGATCCAGAGCTTCTCAAGAGC 900
Qy 301 ArgIysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 901 AGAAGCTAGCCAGGATCGACCTGCGCATCTTGAGCGCTTGGCCATTTGCTGGCTCCA 960
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProIysSerVal 340
Db 961 TACTGCTGTTCACATTTGCTTCACTTACCTTACCAGAAACGGAAGCCCAATCGGTG 1020
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
Db 1021 TGGTACAGATGCTCTTCTGCTGCTGCAATGGTTCATTCGTTGTATCCCTTCTGTAC 1080
Qy 361 ProLeuCyHisArgArgPheGlnIysAlaPheTrpIysIleLeuCyValThrIysTrp 380
Db 1081 CCTTGTGTACAGGCGGCTTCCAGAAAGCTTCTTGGAAGATCTTGTGTGACAAAGCAA 1140
Qy 381 ProAlaLeuSerGlnAsnGlnSerValSerSer 391
Db 1141 CCAGCGCTGTCAAGAACAGTACATCTTCT 1173

RESULT 4
US-10-626-445-6
; Sequence 6, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAS Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-445-6

Alignment Scores:

Pred. No.: 1,35e-182 Length: 1176
Score: 1745.00 Matches: 332
Percent Similarity: 89.26% Conservative: 17
Best Local Similarity: 84.91% Mismatches: 42
Query Match: 85.21% Indels: 0
DB: 20 Gaps: 0

US-10-626-445-8 (1-391) x US-10-626-445-6 (1-1176)

Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProAlaAlaGlnValProLeuAlaPhe 20
Db 1 ATGTGGAGTCTTACCGGCACTGACGTCTTGCCACTGACGTGCTCAATCCCTTTGGCATTT 60
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTATATCTCCCTGCTCTTGTCTATACGATAGCAAGTCGTGTATTTTAAAGCTTT 120
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60

Db 121 GTAGACACAGAAACCTTACATGATGAATATTTTTCCTTAATTTGGCTATTTCT 180
Qy 61 AppPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80
Db 181 GACTTCTTGCGGGTGTATCTCCATTCCTCTGTATCATCCCTCACAGCGTTTAACTGG 240
Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCyThrAla 100
Db 241 AATTTTGGAGAGGATCTGCATGTTTGGCTCATCTGATCTATCTTCTTTGGCACAGA 300
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCGTCTACAGATTTGCTCATTTAGCTACATGATACATCCATCGCTTCAACCGCTGTG 360
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetIysIleValAlaGlnMetValAlaValTrp 140
Db 361 CGTTATAGACACACACACATCGATCCGAAATTTGTTGCTCAATAGTGGCTGTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIysAsnSer 160
Db 421 ATACTGGCTTCTTGTGTCATGCCCCAATGATTCGGCTTCGGAATCTTGGAAAGAACGC 480
Qy 161 ThrAsnTrpIysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180
Db 481 ACCAACACAGAGAGATGAGAGCTGGCTTTGTACTGATGTGTATACCTCTCCCATTACA 540
Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerAlaAlaTyrPheAsnValGlnIleTyr 200
Db 541 GCATCTTGGAATTCCTGCTCCTGCTCTCTGCTGTCGTCGTCATTCATTCAGGTACAGATTTAC 600
Qy 201 TrpSerLeuTrpIysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db 601 TGGACCTGTGTGAMCGTGGAGCTGTCAGTGTGCTCCCTAGCCAGCTGGATTCATCGCT 660
Qy 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 661 ACCTCTTCAGGGGCACTGGACATCTACCGACAGACATGGGTTGGCTTGTAGCAAGTCTT 720
Qy 241 ProGlyLeuIysGluSerAlaAlaSerArgHisSerGluSerProArgArgIysSerSer 260
Db 721 CCTGATTTAAAGAACACGCGCATCCCTTCACTTCAAGAAAGTCCAGAGAAAGACAGT 780
Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheIysValGlySer 280
Db 781 CTCTGCTGTCTCTTAAGACTCACATGAGCGGTACTATCATCGCTTCAAAGTGGGTCC 840
Qy 281 PheTPARSerGluSerAlaAlaLeuArgGlnArgIleValGluLeuLeuArgGly 300
Db 841 TTCTGCCATTCAGAAAGCCAGTGTCTTACCCAGAGAGACAGCTGAGCTTCTCAGAGGC 900
Qy 301 ArgIysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 901 AGAAGCTAGCCAGGATCGCTGAGTGTCTCTCGATGCTTGTGGCATTTGCTGGCTCCG 960
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProIysSerVal 340
Db 961 TATTCCTGTTTCCACATTTGTTTCACTTATCCAGAGGGAGCGGCCCAAAATCGATT 1020
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
Db 1021 TGGTACAGATGCTTCTTGGCTTACAGTGTTCATTTCACTTATTAATCCCTTTCTATAC 1080
Qy 361 ProLeuCyHisArgArgPheGlnIysAlaPheTrpIysIleLeuCyValThrIysTrp 380
Db 1081 CCTTTGTCCACAGACGTTTCCAGAAAGCTTCTTGGAAGATCTGCTGTGACAAAGCAA 1140
Qy 381 ProAlaLeuSerGlnAsnGlnSerValSerSer 391
Db 1141 CCAGCACTTCAACAGACCAGTACATCTTCT 1173

RESULT 5
US-10-626-126-6

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; Sequence 6, Application US/10626126
; Publication No. US2005007470A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNA Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; SOFTWARE: Patent version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-126-6
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Alignment Scores:

Pred. No.:	1,35e-182	Length:	1176
Score:	1745.00	Matches:	332
Percent Similarity:	89.26%	Conservative:	17
Best Local Similarity:	84.91%	Mismatches:	42
Query Match:	85.21%	Indels:	0
DB:	21	Gaps:	0

US-10-626-445-8 (1-391) x US-10-626-126-6 (1-1176)

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QY 1 MetSerGluSerAsnSerThrGlyIleuProProAlaIaGlnValProleuAlaPhe 20
DB 1 ATGTGGAGATCTTAACGGCAGTACGCTCTTCCCTGACCTGACGCTCAAGTCCCTTGGCATTT 60
QY 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleleuAlaPhe 40
DB 61 TTAATGTCCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 120
QY 41 ValIleAlaPheArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
DB 121 GTACGACAGACAAACCTTGTACATCGACAGTAATTAATTTCTTAATTTGGCTAATTTCTT 180
QY 61 AspheLeuValGlyLeuIleSerIleProleuTyrIleProHisValIleuPheAsnTyr 80
DB 181 GACTTCTTGTGGGTCTCATCTTCATCTCTCTGTAATCTCTTCAACGCTGTTAACTGG 240
QY 81 AsnPhenGlySerGlyIleCysMetPheTyrPheIleThrAspTyrLeuLeuCythrAla 100
DB 241 AATTTTGAAGTGAATCTGCAATGTTTGGCTCATTAAGACTATCTTTTGTGCACAGCA 300
QY 101 SerValTyrAsnIleValleuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
DB 301 TCCGCTCAAGTAATGTCTCTCATTAAGTCTGATCGATACGATACGATTCMAACGCTGTG 360
QY 121 SerTyrArgAlaGlnHisThrGlyIleMetCysIleValAlaGlnMetValAlaValTyr 140
DB 361 CGTTATAGACACACACACTGGCATCTCGAATAATTTGTTCTCAAAATGGTGGCTGTTGG 420
QY 141 IleleuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrPlyAsnSer 160
DB 421 ATACTGGCTTTCTTGTGTCATAGGCCCAATGATTCCTGGCTTCGATTCCTGGAAGAACAG 480
QY 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrTyrIleLeuThrIleThr 180
DB 481 ACCAACACAGAGAGAGCGACGCTGCTTGTGTACAGAGTGGTACATCTCCGCAATTACA 540
QY 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
DB 541 GCATTTCTGGAATTCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
QY 201 TrpSerLeuTyrPlyAsnArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
DB 221 TTPSerLeuTyrPlyAsnArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
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DB 601 TGGAGCTCTGTGAAAGCTGGAGCTCTCAGTAGTGCCCTTAAGCCACGCTGATTCATCGCT 660
QY 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
DB 661 ACCTCTTCAGGGGCGACCTGACACTCACGACAGACTGGGTGGCTTGTGAGCAACTCTT 720
QY 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260
DB 721 CCTGATTAAGGAACCAAGCCGATCTCTTCAATTCAGAAAGTCCACGAGGAAGACAGCT 780
QY 261 IleleuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
DB 781 CTCTGGTGTCTTAAAGATCAATGACATGACGGGTGATATATCGCTTCAAAAGTGGGTTC 840
QY 281 PheTyrArgSerGluSerAlaAlaLeuArgGlnArgGlyTyrAlaGlnLeuLeuArgGly 300
DB 841 TTCTGCCGATCAGAAAGCCAGTCTTACACGAGAGACACGTGAGCTTCTCAAGGC 900
QY 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTyrAlaPro 320
DB 901 AGGAGCTAGCCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 321 TyrCysLeuPheThrIleValleuSerTyrTyrProArgThrGluArgProLysSerVal 340
DB 961 TATTCCTGTTCAATATGTTCTTCACTTATCGCAGGGGAGGAGGCCCAATTCGATTT 1020
QY 341 TrpTyrSerIleAlaPheTyrLeuGlnTyrPheAsnSerPheValAsnProPheLeuTyr 360
DB 1021 TGTACAGATAGCTTCTTGGCTACAGTGTCTCAATTCCTTATTAATCTCTTCTTCTTAC 1080
QY 361 ProLeuCyHisArgArgPheGlnLysAlaPheTyrLysIleLeuCyAsnValThrLysTyr 380
DB 1081 CTTTGTGCACAGAGCTTTCAGAGAGCTTCTGGAAGATATCTGTGTGACAAAGCAA 1140
QY 381 ProAlaLeuSerGlyAsnGlnSerValSerSer 391
DB 1141 CCAGCACTTTCACAGACCCAGTCAGTATCTTCT 1173
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RESULT 6

US-10-626-398-6

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; Sequence 6, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNA Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-398-6
```

Alignment Scores:

Pred. No.:	1,35e-182	Length:	1176
Score:	1745.00	Matches:	332
Percent Similarity:	89.26%	Conservative:	17
Best Local Similarity:	84.91%	Mismatches:	42
Query Match:	85.21%	Indels:	0
DB:	21	Gaps:	0

US-10-626-445-8 (1-391) x US-10-626-398-6 (1-1176)

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QY 1 MetSerGluSerAsnSerThrGlyIleuProProAlaIaGlnValProleuAlaPhe 20
DB 1 ATGTGGAGATCTTAACGGCAGTACGCTCTTCCCTGACCTGACGCTCAAGTCCCTTGGCATTT 20
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Db 1 AATGGAGACTTAACGGCACTGCTTTGCCACTGACTGCTCAAGTCCCTTGGCACTT 60
Qy 21 LeuMetSerSerPheAlaPheAlaIleuMetValGlyAsnAlaValIleuAlaPhe 40
Db 61 TTTAATGTCCTGCTTCTTTGCTATAAGATAGGAAGTGTGTATTTAGGCTTT 120
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTAGCAGACAGAAACCTTACATCAACAAATATATTTTCTTAATTTGGCTATTTCT 180
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValIleuPheAsnTyr 80
Db 181 GACTTCTTGTGGGTGATCTTCATCTCTCTGATACATCTCCACACGCTTTTAACTGG 240
Qy 81 AsnPheGlySerGlyIleCysMetPheTyrPheLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 AATTTTGGAAAGTGAATCTGCATGTTTGGCTCATTAGCAGCATCTTTTGGACAGCA 300
Qy 101 SerValTyrAsnIleValIleuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCCGCTCAGATATGCTCTCATAGCTACGATCGATACAGTTCAGTTCAAACGCTGTG 360
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTyr 140
Db 361 CCTTATAGACACAGCACTGGCATCTGAAATATGTTGCTCAAAATGAGTGTGCTTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrLysAsnSer 160
Db 421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATTTGGCTTGGATTTCTTGGAAAGAACGC 480
Qy 161 ThrAsnThrLysAspCysGlnProGlyPheValThrGlnTyrIleLeuThrIleThr 180
Db 481 ACCAACACAGAGAGAGCGAGCGCTGCTTGTATCTAGAGTGTACATCTCCCATTTACA 540
Qy 181 MetLeuLeuGlnPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
Db 541 GCATTTCTGAAATCTGCTCCCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Qy 201 TrpSerLeuTyrLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db 601 TGGACCTGTGGAAGGTGGAGTGTCACTAGTGGCTTACAGCAGCAGCTGATTCATCGT 660
Qy 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 661 ACCCTTTCCAGGGGCACTGGACATCACACAGAACTGGGTGCTTGTAGCAAGTCTT 720
Qy 241 ProGlyLeuLysGlnSerAlaIleSerArgHisSerGlnSerProArgArgLysSerSer 260
Db 721 CCTGATTTAAAGAAACAGCCGCTATCTTCATTCAGAAAGTCCACGAGAAAGAGCACT 780
Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
Db 781 CTCCTGGTGTCTTAAAGATCATCAATGACCGGATGATATGATGCTTCAAATGGGTTCC 840
Qy 281 PheTyrArgSerGlnSerAlaAlaLeuArgGlnArgGlnTyrAlaGlnLeuLeuArgGly 300
Db 841 TTCTGCGCATCAAGAAAGCCAGTGTCTTCACAGAGAGACAGTGGAGCTTCTCAGAGGC 900
Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleGlySerThrAlaPro 320
Db 901 AGGAAGCTAGCAGAGGTGCTAGCTGCTCCCTGAGGCTTTTGGCCATTTGGTGGCTCGG 960
Qy 321 TyrCysLeuPheThrIleValIleuSerThrTyrProArgThrGlnArgProLysSerVal 340
Db 961 TATTGCTCTTCACAATTTCTTTCACTTATCGCAGAGGGAGCGCCCAATCGATTT 1020
Qy 341 TrrTyrSerIleAlaPheTyrLeuGlnTrrPheAsnSerPheValAsnProPheLeuTyr 360
Db 1021 TGGTACAGATAGCTTTTGGCTACAGTGTCTCAATTCATTAATATCCCTTTCTAATC 1080
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrrPylIleLeuCysValThrLysTrr 380
Db 1081 CCTTTGTGCAAGACGTTTCCAGAGGCTTTCTGGAAATATCTCTGTGTGCAAAAGCA 1140

Qy 381 ProAlaLeuSerGlnAsnGlnSerValSerSer 391
Db 1141 CCAGCAGCTTCCACAGACCCAGCAGTCAATCTTCT 1173

RESULT 7

US-09-812-216-1
/ Sequence 1, Application US/09812216
/ Patent No. US20020098539A1
/ GENERAL INFORMATION:
/ APPLICANT: Behan, Jiong Xu
/ APPLICANT: Laz, Thomas M.
/ APPLICANT: Morse, Kelley L.
/ APPLICANT: Umland, Shelby P.
/ APPLICANT: Wang, Suke
/ TITLE OF INVENTION: Histamine receptor
/ FILE REFERENCE: CN01069
/ CURRENT APPLICATION NUMBER: US/09/812,216
/ CURRENT FILING DATE: 2001-03-19
/ PRIOR APPLICATION NUMBER: 09/414,010
/ PRIOR FILING DATE: 1999-10-07
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 1173
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-812-216-1

Alignment Scores:

Pred. No.:	4,39e-141	Length:	1173
Score:	1370.50	Matches:	267
Best Local Similarity:	78.32%	Conservative:	40
Query Match:	68.11%	Mismatches:	82
DB:	9	Indels:	3
		Gaps:	2

US-10-626-445-8 (1-391) x US-09-812-216-1 (1-1173)

Qy 1 MetSerGlnSerAsnSerThrGlyIleuProProAlaIleGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATACCTAAAGACACATCAATTAATCACTACACCTCGGTTACTTACATTT 60
Qy 21 LeuMetSerSerPheAlaPheAlaIleuMetValGlyAsnAlaValIleuAlaPhe 40
Db 61 TTTATGCTCTTAAGTACCTTTTGGCTATATGCTAGGAAATGCTTGTGCTATTTAGCTTT 120
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGGACAAAAACCTTACATGACATGAAAGTATATTTTCTTAACTTGGCCATCTCT 180
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValIleuPheAsnTyr 80
Db 181 GACTTCTTGTGGGTGATCTCCATCTCTTGTATCATCTCCACACGCTGTTCGAATGG 240
Qy 81 AsnPheGlySerGlyIleCysMetPheTyrPheLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGAAATCTGATATTTTGGCTCAGTACATCTCTTATTTGTAACCA 300
Qy 101 SerValTyrAsnIleValIleuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGATATAATCAATTTGCTCATGATGATATGATATGATATGATATGATATGATATG 360
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTyr 140
Db 361 TCTTATAGAACTCAACATATCTGGGTCTTGAAGATTTGTTACTTGATGTGGCCCTTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrLysAsnSer 160
Db 421 GTGCTGCTCTTAAATGAAATGGGCAATGATTTCAATTTCAAGACTTTGGAAAGATGAA 480

OY	161	ThiranthThyAAspCYeGluProGlyPheValThiGluTyrIleLeuThiIeTr	180
Db	481	GGTACT-----GAATGCAACTGGATTTTTTGGAAATGGTACTCTTGGCATCA	534
OY	181	MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIeTyr	200
Db	535	TCAATCTTGGAAATTCGTATCCAGCATCACTTAAGTCGCTTAATTCACATGAATATTAT	594
OY	201	TrpSerLeuTrpLysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr	220
Db	555	TGGAGCCTGTGGAAAGCGTATCATCTTCAGTAAGTGGCAAAAGCATCTTGGACTGACT	654
OY	221	ThrSerSerSerAlaSerGlyHisIleuHisArgAlaGlyValAlaCysArgThrSerAsn	240
Db	655	GTCTCTCCAAATCATCTGTGACACTTCATTCAGAGGTAGACTATCTTCAGAGGATCTTT	714
OY	241	ProGlyLeuLysGluSerLysAlaIleSerArgHisSerGluSerProArgArgLysSerSer	260
Db	715	TCTGCATGCACAGAAATTCCTTCATCTCTTCATTCAGAGACAGAGGAGAAAGATAT	774
OY	261	IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLeuValGlySer	280
Db	775	CTCATGTTTTCTCCAAAGAACCAAGATGATACATACAAATTCCTCCAAAATGGGTTCC	834
OY	281	PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly	300
Db	835	TTCTCCCAATCAGATTCGTACTCTTCCAAAGGAGCAATGTGMACTGCTGTAGAGCC	894
OY	301	ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro	320
Db	895	AGGAAATTAGCAAACTACTGSCCATCTCTTAAAGGGTTTTGCTGTTGCTGGGCTCA	954
OY	321	TyrCysLeuPheThrIleValLeuSerThyTyrProArgThrGluArgProLysSerVal	340
Db	955	TATTCCTCGTCCAAATTCCTTTCATTTTATTCCTCCAGCAACAGGCTCTAAATCAGTT	101
OY	341	TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr	360
Db	1015	TGGTATAGAAATTGCAATTTGGCTTCAGAGGTTCAAATCTTTGTGCATCTCTTTGTAT	107
OY	361	ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThiLysTrp	380
Db	1075	CCATGTGTCAACAAGCGCTTTCAAAGGCTTCTGAAAAATATTTGTATAAAAAGCAA	1133
OY	381	ProAlaLeuSerGln--AsnGlnSerValSerSer	391
Db	1135	CTCTACATCAACAACAGTGGTACAGTATCTTCT	1170

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RESULT 8
US-09-910-411-1
: Sequence 1, Application US/09910411
: Patent No. US20020137054A1
: GENERAL INFORMATION:
: APPLICANT: Bergsma, Berk
: APPLICANT: Filzgerald, Laura
: APPLICANT: Li, Xiaotong
: APPLICANT: Michalovich, David
: APPLICANT: Zhu, Yuan
: TITLE OF INVENTION: AOR35, A G-Protein Coupled Receptor
: FILE REFERENCE: GPT0655-5C1
: CURRENT APPLICATION NUMBER: US/09/910,411
: CURRENT FILING DATE: 2001-07-20
: PRIOR APPLICATION NUMBER: 09/693,761
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 09/497,790
: PRIOR FILING DATE: 2000-02-03
: PRIOR APPLICATION NUMBER: 09/431,898
: PRIOR FILING DATE: 1999-11-02
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 1173
: TYPE: DNA

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ORGANISM: Homo sapien
US-09-910-411-1

Alignment Scores:

Pred. No.:	4,39e-141	Length:	117
Score:	1370.50	Matches:	267
Percent Similarity:	78.32%	Conservative:	40
Best Local Similarity:	68.11%	Mismatches:	82
Query Match:	66.92%	Indels:	3
DB:	9	Gaps:	2

US-10-626-445-8 (1-391) X US-09-910-411-1 (1-1173)

Qy	1	MetSerGluSerAsnSerThrGlyLeuProPheAlaGlnValProLeuAlaPhe	20
Db	1	ATGCCAGATACATGATGACCAATCAATTTCACATGACACTCGGTACTTACCTT	60
Qy	21	LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe	40
Db	61	TTTATGTCCTTAGTAGCTTTTCTCTATTAATGAGCAAAATCGTTGGCATATTTAGCTTTT	120
Qy	41	ValValAspArgAsnLeuArgHisArgSerAsnArgPhePheLeuAsnLeuAlaIleSer	60
Db	121	GTCGTGACAAAACCTTAGACATGAAAGTGTATTTTCTTCACTGGCCACTCT	180
Qy	61	AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr	80
Db	181	GACTTCCTTTGTGGTGATGATCCATTCCTTTGTATGATCCCTCAACAGCGTTGGATGG	240
Qy	81	AsnPheGlySerGlyIleCysMetCysThrLeuIleThrAspTyrLeuLeuCysThrAla	100
Db	241	GATTTTGGAAAGGAATCGTGATATTTTGGCTCACTACGTACTGACTTCGTTATGACGCA	300
Qy	101	SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal	120
Db	301	TCTGTATATACATTTCTCTCATGCTATGATGATGATCCGTGATGCTCAAAAGCTGTG	360
Qy	121	SerTyrArgAlaGlnHisThrGlyIleMetCysIleValAlaGlnMetValAlaValTyr	140
Db	361	TCTTAATAGAACTCAACATCTGGGGCTCTTGAAGATTTGTTACTGTGATGGCGGTTGG	420
Qy	141	IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrAsnSer	160
Db	421	GTCCTGACCTTCTTAGTGATGGGCAATGATTCAGTTTAGAGCTTGGAGAGATGAA	480
Qy	161	ThrAsnThrIysAspCysGluProGlyPheValThrGluTyrTyrIleLeuThrIleThr	180
Db	481	GGAGT-----GAATGTGAACCTGGATTTTTCGGATGTGATCATCTTGGCATACA	534
Qy	181	MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr	200
Db	535	TCATTTTGGAATTCGTGATCCCACTCATCTTAGCGGTTATTTCAACATGATATATTAT	594
Qy	201	TyrSerLeuTyrIysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr	220
Db	595	TGAGCGCTGGAAGCGTATCATCTTCAGTAGGTGCCAAAGCCATCTGGACATGACGCT	654
Qy	221	ThrSerSerAlaSerGlyHisIleuHisArgAlaGlyValAlaCysArgThrSerAsn	240
Db	655	GTCCTTCCAAATCTGTGACACCTCATTCAGAGGTAGATCATTTCCAAAGAGATCTCTT	714
Qy	241	ProGlyLeuLeuGluSerAlaIleSerArgHisSerGluSerProArgArgIysSerSer	260
Db	715	TCTGATCGACAGAAAGTTCCTGCACTCTTCAATTCAGAGACACAGAGAGAAAGATGT	774
Qy	261	IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheIysValGlySer	280
Db	775	CTCATGTTTTCCTCAAGAACCAAGATGATATGCAATATGCTTCCAAAAATGGGTTCC	834
Qy	281	PheTyrArgSerGluSerAlaAlaLeuArgGlnArgIuTyrAlaGluLeuLeuArgGly	300
Db	835	TTCTCCCATCAATGATTCGTAGCTCTTACCAAAAGGAACATGTTGAACGTCTTAGGCC	894

QY 301 ArglySLeuAlaArgSerLeuAlaIleLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTGCGCAAGTCACTGGCATCTTCTTAGGGGTTTGGCTGGGCTGCCA 954
QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGlnArgProLysSerVal 340
Db 955 TATCTCTGTCAACATGTCCTTTCATTTTATCTCTGCAACAGAGCTCTTAATCAGTT 1014
QY 341 TTPYrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
Db 1015 TGGTAGAATTCGATTTTGGCTTCAGTGTTCATCTCTTGTCAATCCTCTTTGTAT 1074
QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
Db 1075 CCATTGTGTCAACAGGCTTTCACAAAGGCTTCTTGAAATATTTGTATATAAAGCAA 1134
QY 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
Db 1135 CCTTACCATCAACACAGCTGCTGATCTTCT 1170

RESULT 9
US-09-875-076-13
; Sequence 13, Application US/09875076
; Publication No. US20030017528A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Kuoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01

; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-076-13

Alignment Scores:
Pred. No.: 4,396-141 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.32% Conservative: 40
Best Local Similarity: 68.11% Mismatches: 82
Query Match: 66.92% Indels: 3
Db: 10 Gaps: 2

US-10-626-445-8 (1-391) x US-09-875-076-13 (1-1173)

QY 1 MetSerGlnSerAsnSerThrGlyIleLeuProAlaAlaGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATACAAATAGCAACATCAATTAATCAGTACAGACCTCGTTACTTACATTT 60
QY 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTTATGCTCTTAAGTACCTTTTGTCTTAATGCTAGAAATGCTTGGTCAATTTACTTTT 120
QY 41 ValValaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGTGGACAAACCTTAGACATGAAAGTATTTTCTTAACTTGGCCATCTCT 180
QY 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80
Db 181 GACTTCTTTGGGGGTGATCTCCATCTCTTGTACATCCCTCACACCGCTGTGAATGG 240
QY 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGAAATCTGTATTTTGGCTCAGTCACTGACTATCTGTATGTACACA 300
QY 101 SerValTyrAsnIleValIleLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATTAACATTTGCTCTCATCAGCTATGATGATACCTGCTCAGTCTCAATCTGTG 360
QY 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrp 140
Db 361 TCTTATAGACATCAACATAGCTGGGCTTGAAGATTTTACTCTGATGCTGCGCTTGG 420
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 GTGCTGGCTCTTCTTAAGTAAATGGCCAAATGATTTCTAGATCTTGAAGAGATGAA 480
QY 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrPyrIleLeuThrIleThr 180
Db 481 GGTACT-----GAATGGAACCTGGATTTTTCGGAATGATACATCTTCCATCA 534
QY 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
Db 535 TCATCTTGAATTCGATCCAGTATCCAGTATCTTACGCTTATTCACATGAAATATTAT 594
QY 201 TrpSerLeuTrpLysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db 595 TGGAGCCGTGGAAGCGGATCATCTCTGTAAGTGGCCAAACCCATCTCGAGACTGCT 654
QY 221 ThrSerSerSerAlaSerGlyHisIleuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 655 GTCTCTTCAACATCTGTGACATCTCAAGAGTAGACTATCTTCAAGAGATCTCTT 714
QY 241 ProGlyLeuLysGlnSerAlaIleSerArgHisArgSerGlnSerProArgArgLysSerSer 260
Db 715 TCTGATCAGACAGAAAGTTCCTGCATCTCTTCAATCAGAGACAGAGAAAGAGTAGT 774
QY 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280

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Db      775 CTCATGTTTCTCAGAAACAGATGAAATGACAAATTCCTTCCAAAATGGGTTCC 834
      281 PHETPARGSERGLUSERALALALAUAGSLNARGLUTYRALGLUENLEUARGGLY 300
      835 TTCCTCCATCATCGATTCCTAGCTTCTTCCACCAAGGAACTTTGAACTGCTTAAGGCC 894
Qy      301 ARGVLEUVALARGSERLEUVALLEULEUSERALAPHEALALECYSTRALAPRO 320
      895 AGGAGATTAGCAAGACACATCGGCATTCTTAGGGGTTTTCCTTGGCTGGCTCCA 954
Db      321 TYRCVLEUPHETHRILLEVALLEUSERTHYRPROARGTHRLUARGPROLYSERVAL 340
      955 TATTCCTGTTCCAAATTCCTTCAATTTATTCCTTCAGCAACAGTCTTAATCAGTT 1014
Qy      341 TTPYRSERLALAPHETRPLEUGINTPPEANSESPHEVALAENPROHELEUTYR 360
      1015 TGGTAGAATTCATTTGGCTTCAGTGGTTCATTCCTTGTCAATCCTCTTTGTAT 1074
Db      361 PROLEUCYHISARGARGPHEGLINLYSALAPHETRPLYSILLEUCYVALTHRLYSTP 380
      1075 CCATTGTGTCACAGGCGTTTCAAAAGCTTTCTTGAATAATTTTGTATAAAAAGCAA 1134
Qy      381 PROALALEUSERGLN--ASGLNSERVALSERSER 391
      1135 CCTTACATCACACACAGTCGTCAGTATCTTCT 1170
Db
RESULT 10
US-09-876-252-13
/ Sequence 13, Application US/09876252
/ Publication No. US20030018182A1
/ GENERAL INFORMATION:
/ APPLICANT: Behan, Dominic P.
/ APPLICANT: Lehmann-Brinema, Karin
/ APPLICANT: Chalmers, Derek T.
/ APPLICANT: Lowitz, Kevin P.
/ APPLICANT: Lin, I-Lin
/ APPLICANT: Dang, Huong T.
/ APPLICANT: Chen, Ruoping
/ APPLICANT: Law, Chen W.
/ TITLE OF INVENTION: Non-Endogenous Constitively Activated Human G Protein Coupled Rec
/ FILE REFERENCE: AREN-0054
/ CURRENT APPLICATION NUMBER: US/09/876,252
/ PRIOR FILING DATE: 2001-06-07
/ PRIOR APPLICATION NUMBER: 09/416,760
/ PRIOR FILING DATE: 1999-10-12
/ PRIOR APPLICATION NUMBER: 09/170,496
/ PRIOR FILING DATE: 1998-10-13
/ PRIOR APPLICATION NUMBER: 60/110,060
/ PRIOR FILING DATE: 1998-11-27
/ PRIOR APPLICATION NUMBER: 60/120,416
/ PRIOR FILING DATE: 1999-02-16
/ PRIOR APPLICATION NUMBER: 60/121,852
/ PRIOR FILING DATE: 1999-02-26
/ PRIOR APPLICATION NUMBER: 60/109,213
/ PRIOR FILING DATE: 1998-11-20
/ PRIOR APPLICATION NUMBER: 60/123,944
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,945
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,948
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,951
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,946
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,949
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/152,524
/ PRIOR FILING DATE: 1999-09-03
/ PRIOR APPLICATION NUMBER: 60/151,114
/ PRIOR FILING DATE: 1999-08-27
/ PRIOR APPLICATION NUMBER: 60/108,029

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/ PRIOR FILING DATE: 1998-11-12
/ PRIOR APPLICATION NUMBER: 60/136,436
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,439
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,567
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/137,127
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/137,131
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/141,448
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: 60/136,437
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/156,555
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/156,634
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/156,653
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/157,280
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,294
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,281
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,282
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/156,633
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/156,633
/ NUMBER OF SEQ ID NOS: 146
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 13
/ LENGTH: 1173
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-876-252-13
Alignment Scores:
Pred. No.: 4,39e-141 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.32% Conservative: 40
Best Local Similarity: 68.11% Mismatches: 82
Query Match: 66.92% Indels: 3
DB: 10 Gaps: 2
US-10-626-445-8 (1-391) x US-09-876-252-13 (1-1173)
Qy      1 MetSerGluSerAsnSerThrGlyIleuProAlaIleValProleuAlaPhe 20
      1 ATGCCAGATCACTAAATGACCAATCAATTTATCACTAAGACACGCTGTTACTTAGCATTT 60
Db      21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValAlaIleuAlaPhe 40
      61 TTTATGTCCTTAGTGTAGCTTTCTTCTAATGCTAAGAAAGCTTGGTCACTTTAGCTTTT 120
Qy      41 ValIleAlaPArgAsnLeuArgHisArgSerAsnTYRPhelPheLeuAsnLeuAlaIleSer 60
      121 GTGGTGACAAATAAAGCTTACATGACATGATGTTATTTTCTTAACTGGCCATCTCT 180
Db      61 AppheLeuValGlyLeuIleSerIleProLeuTYRProHisValLeuPheAsnTrp 80
      181 GACTTCTTGTGGGTGTATCTTCATTTCTTTGTACATCTCCACACGCTGTTCAATGG 240
Qy      81 AasnPhelGlySerGlyIleCysMetPheTrpLeuIleThrAspTYRLeuLeuCYRThrala 100
      241 GATTTTGAAGAAGAAATCTGTATTTTGGCTCACACTGACTATCTGTATGACAGCA 300
Db      101 SerValTYRAsnIleValLeuIleSerTYRAspArgTYRGLNSerValSerAsnAlaVal 120
      301 TCTGTATATTAACATTTGCTTCATGAGCTATGATGATACCTGTGACGTCAATGCTGTG 360

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QY 121 SerTyrArgAlaGlnHisThrGlyTlleMetLysIleValAlaGlnMetValAlaValTyr 140
DB 361 TCTTATAGAACTCAACATATCGGCTTGAAGATGTACTCTGATGTCGCCCTTGG 420
QY 141 IleuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
DB 421 GGTGGCTGCTTCTTGTAGTGAATGGCCAAATGATCTTATGTTTCAAGATCTTGAAGAGTGA 480
QY 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180
DB 481 GGTAGT-----GAATGTAACTGGATTTTTCGATGTGATGATCTCTTGCCATCACA 534
QY 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
DB 535 TCATTCCTTGAATTCCTGATCCAGTCACTTATGCTTATTTTCAACATGAAATTTAT 594
QY 201 TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
DB 595 TGGAGCTGTGGAGGATGATCATCTCAGTAGGTGCCAAAGCCATCTTGGACTGACTGCT 654
QY 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
DB 655 GTCCTTCCAAACATCTGTGACACTCATTCAGAGTAGACTATCTTCAAGAGATCTCT 714
QY 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260
DB 715 TCTGCATCGACAGAGTTCTCGCATCTCTTCATTTCCAGAGAGACAGAGAGAAAGAGTAGT 774
QY 261 IleuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
DB 775 CTCATGTTTCTTCCAGAAACCAAGATGAATAGCAATACATGCTTCCAAATGGATTC 834
QY 281 PheTrpArgSerGluSerAlaAlaLeuArgLysGluTyrAlaGluLeuLeuArgGly 300
DB 835 TTCCTCCAACTAGATTCGTAGCTCTTCCAAAGGAAACATGTGAATGCTTAGAGCC 894
QY 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
DB 895 AGCAATTTAGCCAAAGTCACTGGCCATTCCTTAGAGGGGTTTTCGTGTGGCTGCCA 954
QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
DB 955 TATTCCTGTTCAACATGTCCTTTCATTTTATCTCTCAGCAACAGGCTCTAAATCAGTT 1014
QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
DB 1015 TCGTATAGAAATTCATTTGGCTTCAGTGTTCATTCCTTTGTCAATCCTCTTTGTAT 1074
QY 361 ProLeuCysHisArgArgPheGlnLysValaPheTrpLysIleLeuCysValThrLysTrp 380
DB 1075 CCATTTGTGCACAAAGGCTTTCAAAAGGCTTTCTTGAAAATATTTTGTATAAAAAGCAA 1134
QY 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
DB 1135 CCTTACCATCAACACACAGTCGCTCAGTATCTTCT 1170

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RESULT 11

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US-10-052-193-1
; Sequence 1, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PCI0963A
; CURRENT APPLICATION NUMBER: US/10/052,193
; PRIOR FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-10-052-193-1
Alignment Scores:
Pred. No.: 4,39e-141 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.32% Conservative: 40
Best Local Similarity: 68.11% Mismatches: 82
Query Match: 66.92% Indels: 3
DB: 13 Gaps: 2

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US-10-626-445-8 (1-391) x US-10-052-193-1 (1-1173)

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QY 1 MetSerGluSerAsnSerThrGlyTlleuProProAlaAlaGlnValProLeuAlaPhe 20
DB 1 ATGCAGATACATAAATAGACACATCAATTTATCATTACACACCTCGTTACTTACATTT 60
QY 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40
DB 61 TTTATGTCCTTAGTAGTCTTTTGTATTAATGCTAGAGAAATGCTTGTCAATTTTACCTTT 120
QY 41 ValValaPrgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
DB 121 GTGGTGGCAAAACCTTAGACATGAGTAGTATTTTCTTAACTTGGCCATCTCT 180
QY 61 AsnPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80
DB 181 GACTTCTTGTGGGTGATCTCCATCTCTTGTGATACCTCCACACCGCTTGCATATGG 240
QY 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
DB 241 GATTTTGGAAAGAAATCTGTATTTTGGCTCACTGACTGATCTGTATGATGACGA 300
QY 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
DB 301 TCTGATATTAACATTTGCTCATCAGTATGATGATGATGATGATGATGATGATGATGATG 360
QY 121 SerTyrArgAlaGlnHisThrGlyTlleMetLysIleValAlaGlnMetValAlaValTyr 140
DB 361 TCTTATAGAACTCAACATATCGGCTTGAAGATGTACTCTGATGTCGCCCTTGG 420
QY 141 IleuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
DB 421 GGTGGCTGCTTCTTGTAGTGAATGGCCAAATGATCTTATGTTTCAAGATCTTGAAGAGTGA 480
QY 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180
DB 481 GGTAGT-----GAATGTAACTGGATTTTTCGATGTGATGATCTCTTGCCATCACA 534
QY 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
DB 535 TCATTCCTTGAATTCCTGATCCAGTCACTTATGCTTATTTTCAACATGAAATTTAT 594
QY 201 TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
DB 595 TGGAGCTGTGGAGGATGATCATCTCAGTAGGTGCCAAAGCCATCTTGGACTGACTGCT 654
QY 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
DB 655 GTCCTTCCAAACATCTGTGACACTCATTCAGAGTAGACTATCTTCAAGAGATCTCT 714
QY 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260
DB 715 TCTGCATCGACAGAGTTCTCGCATCTCTTCATTTCCAGAGAGACAGAGAGAAAGAGTAGT 774
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DB 775 CTCATGTTTCTTCCAGAAACCAAGTGAATGCAATACATGCTTCCAAATGGATTC 834
QY 281 PheTrpArgSerGluSerAlaAlaLeuArgLysGluTyrAlaGluLeuLeuArgGly 300
DB 835 TTCCTCCAACTAGATTCGTAGCTCTTCCAAAGGAAACATGTGAATGCTTAGAGCC 894

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QY 301 ArglyLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCyStrPalaPro 320
Db 895 AGGAGATTAGCAAGTCACTGGCCATTCTTAGGGGTTTGGCTGTTCTGGGCTCCA 954
QY 321 TyrCyLeuPheThrIleValIleuSerThrTyrProArgThrGluArgProlySerVal 340
Db 955 TATTCCTGTTCACAAATGCTTCCTTCAATTTATTCCTCAGCAACAGGCTCTAATCAGTT 1014
QY 341 TrpTyrSerIleAlaPheThrLeuGlnTrpPheAsnSerPheValaIleProPheLeuTyr 360
Db 1015 TGGTATATGAAATTCATTTCGCTTCAGTGGTTCATTCTTCCTTCCTTTGAT 1074
QY 361 ProLeuCyHisArgArgPheGlnValaPheThrIleValIleuCyValaIleThrLyStrp 380
Db 1075 CCATTGTGTCAACAGCGCTTTCACAAAGCTTTCCTTGAATAATTTGTATATAAAGCA 1134
QY 381 ProAlaLeuSerGln--AsnGlnSerValSerSer 391
Db 1135 CCTCTACATCACACACAGTCGCTCAGTATCTTCT 1170

RESULT 12
US-10-272-983-13
Sequence 13, Application US/10272983
Publication No. US20030148450A1
GENERAL INFORMATION:
APPLICANT: Chen, Huoping
APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: AREN0050
CURRENT APPLICATION NUMBER: US/10/272,983
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US/09/417,044
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,437
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,567
PRIOR FILING DATE: 1999-05-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapiens
US-10-272-983-13

Alignment Scores:
Pred. No.: 4,39e-141 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.32% Conservative: 40
Best Local Similarity: 68.11% Mismatches: 82
Query Match: 66.92% Indels: 3
DB: 15 Gaps: 2

US-10-626-445-8 (1-391) x US-10-272-983-13 (1-1173)

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QY 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTTATGTCTTACTAGTCTTTGCTATTAATGCGAAAGCTTTGGCTATTTAGCTTTT 120
QY 41 ValIleAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGACAAACAACTTGAACATCGAAGATTAATTTTCTTAACCTTGGCACTCT 180
QY 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
Db 181 GACTCTTTGGGTGTGATCTCCATCTCTTTATACCTCCCTCAGACGCTGTGCAATGG 240
QY 81 AsnPheGlySerGlyIleCyMetPheThrPheIleThrAspTyrIleLeuCyStrPala 100
Db 241 GATTTGGAAAGGAAATCTGTATTTTGGCTCAGTACATCTATCTGTATATGACGA 300
QY 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATACATTTGCTTCATCACTATGATCATCTGCAATCTCCTCAATTCCTGT 360
QY 121 SerTyrArgAlaGlnHisThrGlyIleMetValIleValAlaGlnMetValAlaValTyr 140
Db 361 TCTTATAGAACTCAACATACCTGGGCTTGAAGATTTTACTGTAGTGGCGCTTGG 420
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerThrIleVal 160
Db 421 GTGCTGCTCTTCTTATGATGAGGCGCAATGATTTCTGATTCAGATCTTGAAGATGA 480
QY 161 ThrAsnThrIleAspCyGluProGlyPheValThrGlyTrpTyrIleLeuThrIleTyr 180
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Db 535 TCATCTTGGAAATTCGTGATCCAGATCATCTTATGCTGATTTTCAACATGAATATTAT 594
QY 201 TrpSerLeuThrIleValArgAlaLeuSerArgCyProSerHisAlaGlyPheSerThr 220
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QY 321 TyrCyLeuPheThrIleValIleuSerThrTyrProArgThrGluArgProlySerVal 340
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QY 341 TrpTyrSerIleAlaPheThrLeuGlnTrpPheAsnSerPheValaIleProPheLeuTyr 360
Db 1015 TGGTATATGAAATTCATTTCGCTTCAGTGGTTCATTCTTCCTTCCTTTGAT 1074
QY 361 ProLeuCyHisArgArgPheGlnValaPheThrIleValIleuCyValaIleThrLyStrp 380

PROR FILING DATE: 1999-03-12
PROR APPLICATION NUMBER: 60/123,949
PROR FILING DATE: 1999-03-12
PROR APPLICATION NUMBER: 60/136,436
PROR FILING DATE: 1999-05-28
PROR APPLICATION NUMBER: 60/136,437
PROR FILING DATE: 1999-05-28
PROR APPLICATION NUMBER: 60/136,439
PROR FILING DATE: 1999-05-28
PROR APPLICATION NUMBER: 60/136,567
PROR FILING DATE: 1999-05-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapiens
US-10-393-807-13

Alignment Scores:
Pred. No.: 4,39e-141 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.32% Conservative: 40
Best Local Similarity: 68.11% Mismatches: 82
Query Match: 66.92% Indels: 3
Gaps: 2

US-10-626-445-8 (1-391) x US-10-393-807-13 (1-1173)

QY 1 MetSerGluSerAsnSerThrGlyIleuProAlaIleValProleuAlaPhe 20
DB 1 ATGCCAGATACATTAATGACCAATCAATTTATCTACTAGCACTGCTTACTTACATTT 60
QY 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleuAlaPhe 40
DB 61 TTTATGCTCTTATGATGCTTTTGTCTATTAAGCTAAGAAAGCTTGTGCTTATTAAGCTTTT 120
QY 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnAlaIleSer 60
DB 121 GTGGTGAGCAAAACCTTGACATCGAAGTATTTTCTTAACTTGGCCATCTCT 180
QY 61 AppPheLeuValGlyIleuIleSerIleProLeuTyrIleProHisValleuPheAsnTyr 80
DB 181 GACTCTTGTGGGTGATCTTCATTTCTTGTATCATCCCTCAACGCTGTTCGAATG 240
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DB 301 TCTGTATTAACATTTCTCTCATCACTTATGATCGATCTGCTCACTTCAAAATGCTGTG 360
QY 121 SerTyrArgAlaGlnIleThrGlyIleMetValIleValAlaGlnMetValAlaValTyr 140
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QY 201 TTPSerIleuTyrIleArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
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QY 241 ProGlyLeuGlyGlnSerAlaIleSerArgHisSerGluSerProArgArgIleSerSer 260
DB 715 TCTGATTCACAGAAAGTTCTCTCATCTTCTTCAATTCAGAGGATGATCTTCAAGAGAT 774
QY 261 IleuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheValGlySer 280
DB 775 CTCATGTTTCTTCAAGAACCAAGATGATGATCAATTCATTCCTTCAAAATGGGTTCC 834
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RESULT 15
US-10-417-820A-13
Sequence 13, Application US/10417820A
Publication No. US20030229216A1
GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
APPLICANT: Liaw, Chen W.
APPLICANT: Lowitz, Kevin
APPLICANT: Chalmers, Derek T.
APPLICANT: Behan, Dominic P.
TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
FILE REFERENCE: 7, US28, CON
CURRENT APPLICATION NUMBER: US/10/417, 820A
CURRENT FILING DATE: 2003-04-16
PRIOR APPLICATION NUMBER: 09/416,760
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/110,060
PRIOR FILING DATE: 1998-11-27
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,852
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/123,944
PRIOR FILING DATE: 1999-03-12
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PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,948
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,951
PRIOR FILING DATE: 1999-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 155
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 13
 ; LENGTH: 1173
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-417-820A-13

Alignment Scores:

Pred. No.:	4,39e-141	Length:	1173
Score:	1370.50	Matches:	267
Percent Similarity:	78.32%	Conservative:	40
Best Local Similarity:	68.11%	Mismatches:	82
Query Match:	66.92%	Indels:	3
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US-10-626-445-8 (1-391) X US-10-417-820A-13 (1-1173)

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      1173
QY      41 ValAlaSPARGAsnleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleu 60
      1173
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      1173
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      1173
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QY      81 AsnPheGlySerGlyIleCysMetPheTrpIleuIleThrAspTyrlleuIleuCysThrAla 100
      1173
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DB      301 TCTGATATATACATTTCTCATGACATGACATGACATGACATGACATGACATGACATGACAT 360
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Search completed: October 8, 2005, 06:52:30
 Job time : 894 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2005, 02:09:26 ; Search time 236 Seconds
(without alignments)
8153.650 Million cell updates/sec

Title: US-10-626-445-5

Perfect score: 1176

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Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	686.6	58.4	1173	US-09-414-010-1	Sequence 1, Appl
2	686.6	58.4	1173	US-09-812-216-1	Sequence 1, Appl
3	172.8	14.7	1239	US-09-891-053-2	Sequence 2, Appl
4	172.8	14.7	2700	US-09-891-053-5	Sequence 5, Appl
5	143.2	12.2	1338	US-09-165-543-6	Sequence 6, Appl
6	143.2	12.2	1953	US-09-891-053-26	Sequence 26, Appl
7	143.2	12.2	3244	US-09-165-543-4	Sequence 4, Appl
8	140.4	11.9	1335	US-08-985-090-3	Sequence 3, Appl
9	140.4	11.9	1335	US-09-165-543-3	Sequence 3, Appl
10	140.4	11.9	1335	US-09-167-354-6	Sequence 6, Appl
11	140.4	11.9	1335	US-09-642-855-6	Sequence 6, Appl
12	140.4	11.9	1335	US-09-642-855-6	Sequence 6, Appl
13	140.4	11.9	2050	US-09-891-053-21	Sequence 21, Appl
14	140.4	11.9	2665	US-09-949-016-5059	Sequence 5059, Ap
15	140.4	11.9	2689	US-08-985-090-1	Sequence 1, Appl
16	140.4	11.9	2689	US-09-165-543-1	Sequence 1, Appl
17	140.4	11.9	2699	US-09-167-354-5	Sequence 5, Appl
18	140.4	11.9	2699	US-09-642-855-5	Sequence 5, Appl
19	140.4	11.9	2699	US-09-642-855-5	Sequence 5, Appl
20	94	8.0	1086	US-08-985-090-6	Sequence 6, Appl
21	94	8.0	1086	US-09-165-543-33	Sequence 33, Appl
22	94	8.0	2218	US-08-985-090-4	Sequence 4, Appl
23	94	8.0	2218	US-09-165-543-31	Sequence 31, Appl
24	93.8	8.0	1056	US-09-524-162-1	Sequence 1, Appl
25	72.6	6.2	1893	US-09-891-053-13	Sequence 13, Appl
26	72.6	6.2	9293	US-09-949-016-16801	Sequence 16801, A
27	72	6.1	601	US-09-949-016-17027	Sequence 17027, A

28	67.6	5.7	1401	US-09-826-509-514	Sequence 514, App
29	67.6	5.7	2210	US-09-016-434-1177	Sequence 1177, Ap
30	67.6	5.7	2210	US-10-166-199-1	Sequence 1, Appl
31	64.4	5.5	1599	US-09-826-509-520	Sequence 520, App
32	64.4	5.5	2261	US-09-016-434-1176	Sequence 1176, App
33	61.6	5.2	448	US-09-891-053-12	Sequence 12, Appl
34	61.2	5.2	1233	US-09-721-870-1176	Sequence 1176, App
35	59	5.0	1773	US-09-826-509-516	Sequence 516, App
36	59	5.0	1913	US-09-016-434-1314	Sequence 1314, App
37	57.6	4.9	1579	US-09-016-434-1243	Sequence 1243, Ap
38	56.8	4.8	1440	US-09-826-509-518	Sequence 518, App
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40	56	4.8	1266	US-09-826-509-424	Sequence 424, App
41	56	4.8	1386	US-09-016-434-1339	Sequence 1339, Ap
42	56	4.8	1422	US-09-826-509-512	Sequence 512, App
43	56	4.8	1581	US-08-313-553-8	Sequence 8, Appl
44	56	4.8	1581	US-08-767-993-8	Sequence 8, Appl
45	56	4.8	1956	US-08-313-553-6	Sequence 6, Appl

ALIGNMENTS

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; Sequence 1, Application US/09414010
; Patent No. 6204017
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monama, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/414,010
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-414-010-1

Query Match      58.4%; Score 686.6; DB 3; Length 1173;
Best Local Similarity 75.1%; Pred. No. 6.5e-213;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

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Qy 961 TACTGTCTGTTCACATTTGCTTTCACTTACCCAGAAAGGAGCCCAATGAGTG 1020
Db 955 TATTCCTGTTCACATTTGCTTTCACTTATTCCTCAGCAACAGCTCCTAATACGTT 1014
Qy 1021 TGGTACAGCATTCCTTCTGCTGCAATGCTCAATTCGTTTGTAACTCCCTTGTAC 1080
Db 1015 TGGTATAGAAATTCATTTGGCTTCAAGTGGTCAATTCCTTGTCAATCCTTGTGAT 1074
Qy 1081 CCTTGTGTCAAGGGGCTTCCAGAAAGGCTTCTGAGAAATCTTGTGTGCAAGAA 1140
Db 1075 CCAATGTGTCAAGAGGCTTCAAAAGGCTTCTTGAAATATTTGTATATAAAGCAA 1134
Qy 1141 CCAGCGCTGTCAAGAAC---CAGTCAGTATCTTCTTGA 1176
Db 1135 CCTCTACATCAACACAGACGCTCGTATCTTCTTAA 1173

RESULT 3

US-09-891-053-2
; Sequence 2, Application US/09891053
; Patent No. 6750322

GENERAL INFORMATION:

; APPLICANT: Itadani, Hiraiku
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1239)
US-09-891-053-2

Query Match 14.7%; Score 172.8; DB 4; Length 1239;
Best Local Similarity 49.6%; Pred. No. 2,2e-45;
Matches 562; Conservative 0; Mismatches 557; Indels 15; Gaps 4;

Qy 3 GTGGAGGTCTAAAGTACGTGATCTTGGACAGAGCTGCTCAGGTCCCTTGGCATTTT 62
Db 60 GGGCGCTGCGAGGGGGCGGCGCTTCTGGCTGCTGACCGCTGCTCTGGCTGGCT 119
Qy 63 AATGCTTCAATTTGCTTGTCTAATATGATAGCAATGCTGTGATCTTAAAGCTTTGT 122
Db 120 CATGGGCTGCTCATGTGTGCGACAGTACGGGAAAGGCGCTGTATGTGCGCTTGT 179
Qy 123 GGTGACAGAAACCTTATGACATGAAAGTATTTTCTTAAATTTGGCTATTTTGA 182
Db 180 GGGGATTCGAGCTCGACCCAGAACCACTTCTTGTCTCAACCTCGCATCTTCGA 239

Qy 183 CTTCCTGTGAGGTTTGAATTTCCATTCCTGTACATCCCTCAAGTGTGTTTAAAC---TG 239
Db 240 CTTCCTGTGAGGTTTGAATTTCCATTCCTGTACATCCCTCAAGTGTGTTTAAAC---TG 239
Qy 240 GAAATTTGAAAGTGAATCTGCATGTTTGGCTCATTAATGACTATCTTTTGTGACCCG 239
Db 300 GACCTTCGGAGGGGCTCTGCAAGCTGTGGCTGTGTAAGTACTTACTGTGTCTTC 359
Qy 300 ATCTGTCTCAATATGTTGCTCATTAATGACTATGATGATGATGATGATGATGATGAT 359
Db 360 CTGTGTCTCAATATGTTGCTCATTAATGACTATGATGATGATGATGATGATGATGAT 419
Qy 360 GTCTTAAAGGCTCAACACAGCTGCTCATTAATGATGATGATGATGATGATGATGATGAT 419
Db 420 CTCTTAAAGGCTCAACACAGCTGCTCATTAATGATGATGATGATGATGATGATGATGAT 479
Qy 420 GATACCTGCTTCTTGTAAATGAGCCGATGATTTGCTTCAAG---TTCTTGA 473
Db 480 GGTGCTGGCTTCTCTGTATGAGGCTGCTCAATCTGATGAGGATGATGATGATGATGAT 539
Qy 474 GAAACAGAGAAACAAAGAGCTGTAGGCTGCTTGTAAAGATGATGATGATGATGATGAT 533
Db 540 CAGTTCATTCCTGAGAGGCTGCTGTAGGCTGCTTGTAAAGATGATGATGATGATGATGAT 599
Qy 534 CATTAAGATGCTTGTGAATTCCTGCTGCTGTATCTGTGCTTATTTCAATGTAGA 593
Db 600 CAGGCTCTCAACCTGTGATGCTTCAAGCTTCTCAAGCTTCTTCAAGCTTCAAGCT 659
Qy 594 GATTACTGAGAGCTGTGAAGGCTCTCAAGGCTCTCAAGGCTCTCAAGGCTCTCAAGG 653
Db 660 CATCTACATGAAATCATCAAGAGGCTGCTGCTTGTAAAGATGATGATGATGATGATGAT 719
Qy 654 CTCTCAATCTCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGG 713
Db 720 CCAGAAACCCCAACAGAGCTGCTGCTGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGG 779
Qy 714 AAGTAACTCTGATTAAGAAATCAAGCTGCTCTGCTCAAGGCTTCAAGGCTTCAAGG 773
Db 780 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 839
Qy 774 GAGCAGCATCTGCTGCTGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGG 833
Db 840 GGGCACTGAGAGGCTGCTGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGG 896
Qy 834 GGGTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 893
Db 897 ATCTGAGAGAGCTGATGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 956
Qy 894 CAGAGCAGAGAGCTGAGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 953
Db 957 GCGGACAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1016
Qy 954 GGTCTCATCTGTGCTTCAATGCTTCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGG 1013
Db 1017 GGGCGCTGACAGCTCTTCAATGCTTCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGG 1076
Qy 1014 ATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1073
Db 1077 TT---ACTGTATGAGAGCTGCTTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCT 1133
Qy 1074 TCTGTACCTTGTGTCAAGGCTTCTGAGAAAGGCTTCTGAGAAATCTTTG 1127
Db 1134 CCTTACCACTGTGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1187

RESULT 4

US-09-891-053-5
; Sequence 5, Application US/09891053
; Patent No. 6750322

GENERAL INFORMATION:

; APPLICANT: Itadani, Hiraiku
; APPLICANT: Takimura, Tetsuo

APPLICANT: Nakamura, Takao
APPLICANT: Kobayashi, Masahiko
APPLICANT: Tanaka, Ken-ichi
APPLICANT: Hidaka, Yuseuke
APPLICANT: Ohta, Masataka
TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
FILE REFERENCE: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
CURRENT FILING DATE: 06501-083001
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US/09/891,053
PRIOR FILING DATE: 1999-12-24
PRIOR APPLICATION NUMBER: PCT/JP98/05967
PRIOR FILING DATE: 1998-12-25
PRIOR APPLICATION NUMBER: JP 11/145661
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 2700
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: CDS
LOCATION: (351)...(1589)
NAME/KEY: misc_feature
LOCATION: (1)...(2700)
OTHER INFORMATION: n = A,T,C or G
US-09-891-053-5

Query Match 14.7%; Score 172.8; DB 4; Length 2700;
Best Local Similarity 49.6%; Pred. No. 3.6e-45;
Matches 562; Conservative 0; Mismatches 557; Indels 15; Gaps 4;

3 GTCCGAGTCTACAGATCTGAGATCTTGGACACAGCTGCTCAGTCCCTTGGCATTCTT 62
410 GCGGCGTGAAGCGGGGCGCGGCTTCTGCGTGTGCGACCGCTGTCTGCGGCT 469
63 AATGCTTCAATTTGCTTGTATTAATGATGAGCAATGCTGATCTTATGCTTGT 122
470 CATGGCGCTGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 529
123 GGTGACAGAACTTGAACATGAAATTAATTTTCTTAATTTGGCTAATTTTGA 182
530 GCGGATTCAGACCTCCGACCCAGAACTTCTTCTGCTCAACCTGCGCATCTCGA 589
183 CTTCCTGCGGTTGATTTCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 239
590 CTTCCTGCGGTTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 649
240 GATTTTGAAGTGAATCTGATGATTTTGGCTCATTTACTGATCTTTTGGACCGC 299
650 GACCTTCGCGCGGCGCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 709
300 ATCTGCTCAATATTTCTCTAATTAAGTCAATGATGATGATGATGATGATGAT 359
710 CTGCGCTTCAACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 769
360 GCTTATAGGCTGCAACACATGCTGATGATGATGATGATGATGATGATGATGAT 419
770 CTCTCAAGGCGCGCGAGGAGACGAGACGCGCGCTTCCGAGATGACCTGGTGG 829
420 GATCTGCTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 473
830 GGTGCTGCGCTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 889
474 GAAACGACAAACAAAGAGCTGAGCTTGGCTTTGTTAAGAGTGTATCTCTAC 533
890 CAGTTCATCCCGAGGCGCAGCTGATGATGATGATGATGATGATGATGATGAT 949
534 CATTCAGATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 593
950 CAGGCTCTCAACCTTGAAGTTTCAAGCGCTTCTCAAGCGTTTCACTTCAACCT 1009

594 GATTACTGAGCCTGTGAGAGCTGAGGCTTCTAGTAGTCCCTAGCCATGTGAT 653
1010 CATTCACCGAATCAGAGAGCGGACCGGCTTGTGATGAGGCGGTGAGGCTG 1069
654 CTCCATCTCTTCTTCAAGCTTCTGAGACCTTCAACAGAGCTGGGCTGCTGAGAC 713
1070 CCCAAGACCCCAAGATGCCAGCCCTGCGCACCTCCAGCTCCCGGCTGGGG 1129
714 AGTAATCTGATTTGAAGATCAGCTGATCTGTCACTGAGAAAGCTTCAAGANA 773
1130 CTGCGGCAAGAGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1189
774 GAGCAGATCTGCTGCTTCTTAAAGACTCAATGAAACAGCACTGCTTCAAGT 833
1190 GGGCAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1246
834 GGGTCTCTTCTGCGATGCGAAAGTGCAGCGCTTGGCCAAAGGAGTACGAGCTT 893
1247 ATCCCTGAGAAAGCCATGAGATGATGATGATGATGATGATGATGATGATG 1306
894 CAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 953
1307 GCGGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1366
954 GGGTCAATCTGCTGCTTCAATGATGATGATGATGATGATGATGATGATGAT 1413
1367 GCGGCGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1426
1014 ATGCGTGTGATGAGATGATGATGATGATGATGATGATGATGATGATGATG 1073
1427 TT---ACGTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1483
1074 TCTGATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1127
1484 CTTTACCATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1537

RESULT 5
US-09-165-543-6
Sequence 6, Application US/09165543
Patent No. 6093545
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: NNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)742-4214
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 1338 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1335
US-09-165-543-6

Query Match 12.2%; Score 143.2; DB 3; Length 1338;
Best Local Similarity 54.2%; Pred. No. 1e-35;
Matches 339; Conservative 0; Mismatches 278; Indels 9; Gaps 2;

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QY 3 GTGGAGTCTAACAAGTACTGTCATCTTGGCCACGAGCTGCTCAGGTCCCTTGGCATTTT 62
DB 60 GGGGGCTGACAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
QY 63 AATGCTTCAATTTGCTTCTTCTAATATGTAAGCAATGCTGAGTCACTTAAAGCTTTGT 122
DB 120 CATGGGGCTGCTCATCTGTCGACAGTACTGGGCAAGCGCTGTATGCTCCGCTTGT 179
QY 123 GGTGACAGAAACCTTAAGACATGAAATTAATTTTCTTAATTGGCTAATTCTGA 182
DB 180 GGGGAGTTGAGGCTCCGACCCAGAACACTTCTTCTGCTCAACTCGCATCTCGA 239
QY 183 CTTCCTCGTGGGTTTATTTCCATCTCTGTATACCTCTCAAGTGTGTTTAAAC--TG 239
DB 240 CTTCCTCGTGGGTTTATTTCCATCTCTGTATACCTCTGTATACCTCTGTATACCTG 299
QY 240 GAATTTTGAAGTGAATCTGATGTTTGGCTCATTAAGTACTATCTTTTGGACCGC 289
DB 300 GACCTTCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
QY 300 ATCTGTCTAATATTTGCTTCTAATATGTAAGCAATGCTGAGTTCCTTCAATGCTGT 359
DB 360 CTGGGCTTCAATCATGTAATCAATGTAAGCAATGCTGAGTTCCTTCAATGCTGT 419
QY 360 GTCTTAAAGGGCTCAACACATGTCATGAAATTTGCTCAATGTTGGCTGTTTG 419
DB 420 CTCTTCAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
QY 420 GATCTGCTTTCTTGGTAAATGAGCCGATGATTTCTGCTTCAAG--TTCTTGA 473
DB 480 GGTGCTGGCTTCTCTGTATGAGGCTGCTGATCTGAGTTGGAGTACCTGCTGTGG 539
QY 474 GAACAGCAGAACAAAGAGCTGTAGCTGCTGCTTGTAAAGAGTGAATCTCTAC 533
DB 540 CAGTTCATCCCGAGGGGCACTGTATGCTGAGTTCTTCAACAGTGAATTTCTCAT 599
QY 534 CATTACAATGCTTTGGAATTTCTGCTTCTGTATCTGTGGCTTATTTCAATGTA 593
DB 600 CAGGGCTTCACCTCGAGTTCTTCAAGCCCTTCTCAGGCTTAACCTTTCAACCTCAG 659
QY 594 GATTACTGAGGCTGTGGAAGCTA 619
DB 660 CATCTACCTGAACATCCAGAGGGCA 685
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RESULT 6

US-09-891-053-26
Sequence 26, Application US/09891053
Patent No. 6750322
GENERAL INFORMATION:
APPLICANT: Itadani, Hiraiku
APPLICANT: Takimura, Tetsuo
APPLICANT: Nakamura, Takao
APPLICANT: Kobayashi, Masahiko
APPLICANT: Tanaka, Ken-ichi
APPLICANT: Hidaka, Yusuke
APPLICANT: Ohta, Masataka
TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)

TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
FILE REFERENCE: 06501-083001
CURRENT APPLICATION NUMBER: US/09/891,053
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: PCT/JP99/07280
PRIOR FILING DATE: 1999-12-24
PRIOR APPLICATION NUMBER: PCT/JP98/05967
PRIOR FILING DATE: 1998-12-25
PRIOR APPLICATION NUMBER: JP 11/145661
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 1953
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: CDS
LOCATION: (302)...(1636)
US-09-891-053-26

Query Match 12.2%; Score 143.2; DB 4; Length 1953;
Best Local Similarity 54.2%; Pred. No. 1.3e-35;
Matches 339; Conservative 0; Mismatches 278; Indels 9; Gaps 2;

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QY 3 GTGGAGTCTAACAAGTACTGTCATCTTGGCCACGAGCTGCTCAGGTCCCTTGGCATTTT 62
DB 361 GGGGGCTGACAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
QY 63 AATGCTTCAATTTGCTTCTTCTAATATGTAAGCAATGCTGAGTCACTTAAAGCTTTGT 122
DB 421 CATGGGGCTGCTCATCTGTCGACAGTACTGGGCAAGCGCTGTATGCTCCGCTTGT 480
QY 123 GGTGACAGAAACCTTAAGACATGAAATTAATTTTCTTAATTGGCTAATTCTGA 182
DB 481 GGGGAGTTGAGGCTCCGACCCAGAACACTTCTTCTGCTCAACTCGCATCTCGA 540
QY 183 CTTCCTCGTGGGTTTATTTCCATCTCTGTATACCTCTCAAGTGTGTTTAAAC--TG 239
DB 541 CTTCCTCGTGGGTTTATTTCCATCTCTGTATACCTCTGTATACCTCTGTATACCTG 600
QY 240 GAATTTTGAAGTGAATCTGATGTTTGGCTCATTAAGTACTATCTTTTGGACCGC 299
DB 601 GACCTTCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
QY 300 ATCTGTCTAATATTTGCTTCTAATATGTAAGCAATGCTGAGTTCCTTCAATGCTGT 359
DB 661 CTGGGCTTCAATCATGTAATCAATGTAAGCAATGCTGAGTTCCTTCAATGCTGT 720
QY 360 GTCTTAAAGGGCTCAACACATGTCATGAAATTTGCTCAATGTTGGCTGTTTG 419
DB 721 CTCTTCAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
QY 420 GATCTGCTTTCTTGGTAAATGAGCCGATGATTTCTGCTTCAAG--TTCTTGA 473
DB 781 GGTGCTGGCTTCTCTGTATGAGGCTGCTGATCTGAGTTGGAGTACCTGCTGTGG 840
QY 474 GAACAGCAGAACAAAGAGCTGTAGCTGCTGCTTGTAAAGAGTGAATCTCTAC 533
DB 841 CAGTTCATCCCGAGGGGCACTGTATGCTGAGTTCTTCAACAGTGAATTTCTCAT 900
QY 534 CATTACAATGCTTTGGAATTTCTGCTTCTGTATCTGTGGCTTATTTCAATGTA 593
DB 901 CAGGGCTTCACCTCGAGTTCTTCAAGCCCTTCTCAGGCTTAACCTTTCAACCTCAG 960
QY 594 GATTACTGAGGCTGTGGAAGCTA 619
DB 961 CATCTACCTGAACATCCAGAGGGCA 986
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RESULT 7

US-09-165-543-4
Sequence 4, Application US/09165543

Patent No. 6093545
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3244 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 778..2112
US-09-165-543-4

Query Match 12.2%; Score 143.2; DB 3; Length 3244;
Best Local Similarity 54.2%; Pred. No. 1.8e-35;
Matches 339; Conservative 0; Mismatches 278; Indels 9; Gaps 2;

3 GTCCGAGCTTAACAGTCTGATCTTGGCACAGCTGCTGACAGTCCCTTGGCATTTT 62
837 GCGCGCTGAGGCGGCGCGCGGCTTCTGCGCTGCTGACCGCTGCTGCGCT 896
63 AATGCTTCAATTCCTTGTATTAATGAGCAATGCTGATCTTAGCTTGT 122
897 CATGGCGCTGCTGATGCTGCGCAAGTATGCGCAAGCGGCTGCTATCTGCTTGT 956
123 GGTGACAGAAACCTTAGACATGCAAGTAATATTTTCTTAATTTGGCTATTTCGA 182
957 GCGGATTCGAGCCTCCGACCCAGAACAATCTTCTGCTCAACCTGCGCATCCGA 1016
183 CTTCCTCGGGTTGATTTCAATTCCTGTAACCTCCCTCAAGCTTTTAAAC---TG 239
1017 CTTCCTCGGGTGGCTTCTGATTCCTGATTCGATCCCTTAAGTGTACCGCGTTG 1076
240 GAATTTGAGATGAGATCTGATGATTTTGGCTCAATTAATCTTTGGACCGC 299
1077 GACCTTCGCGCGGCGGCTCTGCAAGCTGTGCTGGTGTAGACTACTGTGTGCTTC 1136
300 ATCTGTCAAAATTTGCTTCAATTAAGTACGATGCAACAGTCAATTTCAATGCTGT 359
1137 CTGGGCTTCAACATGTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1196
360 GTCTTAATGGGCTCAACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 419

1197 CTCCTACAGGCGCCACAGCAGGCGGACACAGACAGGCGCTTGGAAAGATGCACTGTGTG 1256
420 GATACGTGCTTCTTGTATTAATGAGCCCGATGATTCGTGCTTCAGA-----TTCTTGAA 473
1257 GGTGCTGCGCTTCTGCTGATGATGAGGCTGCGCATCTGATGAGAGTACCTGTGTGG 1316
474 GACAGCAGCAACAGAAAGAGTGTGAGCTGCGCTTTGTATACAGATGATCTCTAC 533
1317 CAGTTCATCCCGGAGGCGCACTGCTATGCTGAGTCTTCAACAATGATCTTCTCAT 1376
534 CATTAATGATCTTGAATTCCTGCTTCTGCTGATCTCTGTGCTTAATTAATGATGACA 593
1377 CAGGCTTCACACCTTCGAGTTCCTTACGCGCTTCTTCAAGCTTCTTCAACTCAG 1436
594 GATTTACTGAGCCTGTGGAAGCTTA 619
1437 CATCTACCTGAACATCCAGAGCGCA 1462

RESULT 8
US-08-985-090-3
Sequence 3, Application US/08985090
Patent No. 5885893
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,090
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jean M. Silveri
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1335
US-08-985-090-3

Query Match 11.9%; Score 140.4; DB 2; Length 1335;
Best Local Similarity 53.6%; Pred. No. 8.4e-35;
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

3 GTCCGAGCTTAACAGTCTGATCTTGGCACAGCTGCTGACAGTCCCTTGGCATTTT 62
60 GCGCGCGGCGGCGGCGGCGGCTTCTGCGAGCTGACCGCGGCTGCGCGCGCT 119
63 AATGCTTCAATTCCTTGTATTAATGAGCAATGCTGATCTTAGCTTGT 122

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Db 120 CATGGCCCTGCTCATCTGCGCCACGCGTGTGGGCAACGCGCTGTGCTGCTCGCTTGT 179
Qy 123 GGTGGACAGAACTTATAGACATGGAATATATTTTCTTAATTTGGCTATTTCTGA 182
Db 180 GGGCGACTCGAGCTCCGACCCAGAACTTCTTCTCTCAACCTCGCATCTCGA 239
Qy 183 CTTCCTGCTGGGTTTGAATTTCTATCTCTGTACATCCCTCAGCGTGTG---TTTAATG 239
Db 240 CTTCCTGCTGGGCGCTTCTGATCCCATCTGTATGTACCTACCTGTGTACAGCGCGCTG 239
Qy 240 GAATTTTGGAGTGAATCTGCAATGTTTGGCTTCACTGACTATCTTTTGTGACCGC 239
Db 300 GACCTTCGCGCGGGGCTCTGCAAGCTGTGGTGTGTGAGACTACCTGCTGTGACCTC 359
Qy 300 ATCTGTCTCAATATTTGCTCTCACTTATGACTAGATGATACAGTCACTTCAATATGCTG 359
Db 360 CTTCGCTTCAACATCTGTCTCATCACTGATGACCGCTTCTGTGTGACCGGAGCGGT 419
Qy 360 GTCTTATAGGCTCAACACACTGCGCATCATGAATGTTGCTCAATGTGCGCTTTTG 419
Db 420 CTGATACCGGGGCCAGAGGGTGAACGCGGGCGGAGTGGAGAAATGCTGTGTGTG 479
Qy 420 GATACCTGCTTTCTTGTGTAATGCGCCGATGATTTGCTTCAAGT-----TCTTGGAA 473
Db 480 GGTGCTGGCTCTCTGCTGTACGGAACGACCATCTGAGCTGGGAGTACCTGTCCGGGG 539
Qy 474 GAACAGACAGAACAAAGAGACTGTGAGCTGTGTTGTACAGAGTGTACATCTCTAC 533
Db 540 CACCTTCATCCCGAGGGCCACTGTATGCGAGTTCTTTCACACATGTAATCTCTCAT 539
Qy 534 CATTACAATCTCTTGAATTTCTGCTTCTGTATCTGTGAGCTTATTTCAATGTACA 533
Db 600 CAGGCTTCAACCTCTGAGTTCTTTAGCGCTTCTTCAAGGCTACCTTTTAACTCAG 659
Qy 594 GATTACTGAGCGCTGTGAGCGTGAAGCGTGAAGCGCTTCTCAG 629
Db 660 CATCTACCTGATCATCCAGAGCGGACCCGCTCCG 695

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RESULT 9
US-09-165-543-3
Sequence 3, Application US/09165543
Patent No. 6093545
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNT-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400

```

TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1335
US-09-165-543-3
Query Match 11.9%; Score 140.4; DB 3; Length 1335;
Best Local Similarity 53.6%; Pred. No. 8.4e-35;
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;
Qy 3 GTCCGAGTCTTACAGTATGCGCATCTTGGCCACCAAGCTGCTCAGGTCCTTGGCATTTT 62
Db 60 GCGCGCGCGCGCGCGCGCGCGCGCTTCTGCGCAGCTGAGACCGCGAGTCCGCGCT 119
Qy 63 AATGCTTCAATTGCTTGTCTATTAATGAGGCAATGCTGTGATCTTGTGCTTGT 122
Db 120 CATGGCGCTGCTCATGTGCGCACGAGTGTGGGCAACGCGTGTATGCTGCTTGT 179
Qy 123 GGTGGACAGAACTTATAGACATGGAATATATTTTCTTAATTTGGCTATTTCTGA 182
Db 180 GGGCGACTCGAGCTCCGACCCAGAACTTCTTCTGTCTACACTGCGCATCTCCGA 239
Qy 183 CTTCCTGCTGGGTTTGAATTTCTATCTCTGTACATCCCTCAGCGTGTG---TTTAATG 239
Db 240 CTTCCTGCTGGGCGCTTCTGATCCCATCTGTATGTATGACTGACAGCGCGCTG 239
Qy 240 GAATTTTGGAGTGAATCTGCAATGTTTGGCTTCACTGACTATCTTTTGTGACCGC 239
Db 300 GACCTTCGCGCGGGGCTCTGCAAGCTGTGAGCTGTGATGAGTACCTGTGTGACCTC 359
Qy 300 ATCTGTCTCAATATTTGCTCTCACTTATGACTAGATGATCAAGTCACTTCAATGCTGT 359
Db 360 CTTCGCTTCAACATGTGTCTCATCACTGATGACACCGCTTCTGTGCTACCCGAGCGGT 419
Qy 360 GTCTTATAGGCTCAACACACTGCGCATCATGAATGTTGCTCAATGTGCGCTTTTG 419
Db 420 CTGATACCGGGGCCAGAGGGTGAACGCGGGCGGAGTGGAGAAATGCTGTGTGTG 479
Qy 420 GATACCTGCTTTCTTGTGTAATGCGCCGATGATTTGCTTCAAGT-----TCTTGGAA 473
Db 480 GGTGCTGGCTTCTCTGCTGTACGGAACGACCATCTGAGCTGGAGTACCTGTCCGGGG 539
Qy 474 GAACAGACAGAACAAAGAGACTGTGAGCTGTGTTGTACAGAGTGTACATCTCTAC 533
Db 540 CACCTTCATCCCGAGGGCCACTGTATGCGAGTTCTTTCACACATGTAATCTCTCAT 539
Qy 534 CATTACAATCTCTTGAATTTCTGCTTCTGTATCTGTGAGCTTATTTCAATGTACA 533
Db 600 CAGGCTTCAACCTCTGAGTTCTTTAGCGCTTCTTCAAGGCTACCTTTTAACTCAG 659
Qy 594 GATTACTGAGCGCTGTGAGCGTGAAGCGTGAAGCGCTTCTCAG 629
Db 660 CATCTACCTGATCATCCAGAGCGGACCCGCTCCG 695

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RESULT 10
US-09-167-354-6
Sequence 6, Application US/09167354A
Patent No. 6136559
GENERAL INFORMATION:
APPLICANT: Lovenberg, Timothy
APPLICANT: Erlander, Mark
APPLICANT: Pyati, Jayaashree
APPLICANT: Huvac, Arne
TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
TITLE OF INVENTION: SUBTYPE

```
FILE REFERENCE: JMW
CURRENT APPLICATION NUMBER: US/09/167,354A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 1335
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-167-354-6
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Query Match      11.9%; Score 140.4; DB 3; Length 1335;
Best Local Similarity 53.6%; Pred. No. 8.4e-35;
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;
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QY      3 GTGGAGCTTAAAGATCTGATCTTGGCCACGAGTGTCCCTTGCAATTTT 62
DB      60 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 119
QY      63 AATGCTTCAATTTGCTTGTCTAATAAGTAGCAATGTGTGATCTTAAGCTTTGT 122
DB      120 CATTGGGCTGTCTCATGTGGCCACGGTGTGGGCAAGCGCTGTATGTGCTTGGT 179
QY      123 GGTGACAGAAACCTTGAACATGAAATTAATTTTCTTAATTTGGCTAATTTTGA 182
DB      180 GGGCGACTGAGCTCCGACCCAGAAACAATCTTCTGCTCAACCTGCGCATCTCCGA 239
QY      183 CTTCCTGGGGTTTGAATTTTCAATCTGCTGTAACCTCCAGAGTTG---TTTAAC 239
DB      240 CTTCCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 299
QY      240 GAATTTGGAAGTGAATCTGATCTTGGCTCATTAAGTATCTTTTGTGACCGC 299
DB      300 GACCTTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 359
QY      300 ATCTGCTCAATATTTGCTCTCAATTAAGTACATGATGATCAAGTTTCAATGCTGT 359
DB      360 CTCTGCTTCAACATGCTGCTCATGCTACGACCGCTTCTGCTGCTGACCGGCGGT 419
QY      360 GTCTTAAGGGGTCACACACGCGCATGAAAGATTTGTCTCAATAGTGTGCTTTG 419
DB      420 CTCATACCGGGGCCACAGGGGTACACGGGGGGGGGAGGAAATCTGTGTGTG 479
QY      420 GATTAAGGCTTTCTTGTAAATGCGCGATGATCTGAGTTGAGT-----TCTTGA 473
DB      480 GGTGCTGGCTTCTGCTGTAAATGCGCGATGATCTGAGTTGAGT-----TCTTGA 473
QY      474 GAACAGCAGAACACAAAGACTGTGAGCTGTGCTTTGTTACAGATGTGATCTCTAC 533
DB      540 CAGCTTCATCCCGGAGGGCCACTGCTATGCCGATCTTCTCAACATGCTACTCTCAT 599
QY      534 CATTAACAATGCTTGTGAATTCCTGCTTCTGTCATCTGTGCTTATTTCAATGTACA 593
DB      600 CACGGCTTCAACCTCGAGGTTCTTTAGGCTTCTTCCAGCGTCACTTCTTAACCTCAG 659
QY      594 GATTTACTGGAAGCTGTGAAAGCGTAGGGCTCTCAG 629
DB      660 CATCTACCTGAACATCCAGAGGGGACCGGCTCTCG 695
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RESULT 11
US-09-642-855-6

Sequence 6, Application US/09642855

Patent No. 643743

GENERAL INFORMATION:

APPLICANT: Lovenberg, Timothy

APPLICANT: Brlander, Mark

APPLICANT: Pyati, Jayashree

APPLICANT: Huvar, Arne

TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3

SUBTYPE

```
FILE REFERENCE: JMW
CURRENT APPLICATION NUMBER: US/09/642,855
CURRENT FILING DATE: 2000-08-21
PRIORITY APPLICATION NUMBER: 09/167,354
PRIORITY FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 1335
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-855-6
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Query Match      11.9%; Score 140.4; DB 3; Length 1335;
Best Local Similarity 53.6%; Pred. No. 8.4e-35;
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;
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QY      3 GTGGAGCTTAAAGATCTGATCTTGGCCACGAGTGTCCCTTGCAATTTT 62
DB      60 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 119
QY      63 AATGCTTCAATTTGCTTGTCTAATAAGTAGCAATGTGTGATCTTAAGCTTTGT 122
DB      120 CATTGGGCTGTCTCATGTGGCCACGGTGTGGGCAAGCGCTGTATGTGCTTGGT 179
QY      123 GGTGACAGAAACCTTGAACATGAAATTAATTTTCTTAATTTGGCTAATTTTGA 182
DB      180 GGGCGACTGAGCTCCGACCCAGAAACAATCTTCTGCTCAACCTGCGCATCTCCGA 239
QY      183 CTTCCTGGGGTTTGAATTTTCAATCTGCTGTAACCTCCAGAGTTG---TTTAAC 239
DB      240 CTTCCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 299
QY      240 GAATTTGGAAGTGAATCTGATCTTGGCTCATTAAGTATCTTTTGTGACCGC 299
DB      300 GACCTTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 359
QY      300 ATCTGCTCAATATTTGCTCTCAATTAAGTACATGATGATGATCAAGTTTCAATGCTGT 359
DB      360 CTCTGCTTCAACATGCTGCTCATGCTACGACCGCTTCTGCTGCTGACCGGCGGT 419
QY      360 GTCTTAAGGGTCAACACATGCGCATGAAAGATTTGTCTCAATAGTGTGCTTTG 419
DB      420 CTCATACCGGGGCCACAGGGGTACACGGGGGGGGGAGGAAATCTGTGTGTG 479
QY      420 GATTAAGGCTTTCTTGTAAATGCGCGATGATCTGAGTTGAGT-----TCTTGA 473
DB      480 GGTGCTGGCTTCTGCTGTAAATGCGCGATGATCTGAGTTGAGT-----TCTTGA 473
QY      474 GAACAGCAGAACACAAAGACTGTGAGCTGTGCTTTGTTACAGATGTGATCTCTAC 533
DB      540 CAGCTTCATCCCGGAGGGCCACTGCTATGCCGATCTTCTCAACATGCTACTCTCAT 599
QY      534 CATTAACAATGCTTGTGAATTCCTGCTTCTGTCATCTGTGCTTATTTCAATGTACA 593
DB      600 CACGGCTTCAACCTCGAGGTTCTTTAGGCTTCTTCCAGCGTCACTTCTTAACCTCAG 659
QY      594 GATTTACTGGAAGCTGTGAAAGCGTAGGGCTCTCAG 629
DB      660 CATCTACCTGAACATCCAGAGGGGACCGGCTCTCG 695
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RESULT 12
US-09-642-514-6

Sequence 6, Application US/09642514

Patent No. 6437100

GENERAL INFORMATION:

APPLICANT: Lovenberg, Timothy

APPLICANT: Brlander, Mark

APPLICANT: Pyati, Jayashree

APPLICANT: Huvar, Arne


```

? TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
? FILE REFERENCE: SUBTYPE.
? FILE REFERENCE: CRT1290
? CURRENT APPLICATION NUMBER: US/09/642,514
? CURRENT FILING DATE: 2000-08-21
? PRIOR APPLICATION NUMBER: US 09/167,354
? PRIOR FILING DATE: 1998-10-06
? NUMBER OF SEQ ID NOS: 8
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 6
? LENGTH: 1335
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-642-514-6

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Query Match	11.9%	Score 140.4;	DB 3	Length 1335;
Best Local Similarity	53.6%	Pred. No. 8.4e-35;		
Matches 341; Conservative	0;	Mismatches 286;	Indels 9;	Gaps 2

QY	3	GTCCGAGCTCAACATGATCTGGCATCTTGGCACAAGCTGCTCAGAGTCCCTTGGCATTTT	62
Db	60	GGCCGCGCGGGCGGGGCGCGGGCTTCTCCGCAAGCTTGACCCGCGGTGGCCGGCCT	119
QY	63	AATGCTTCAATTGGCTTGTCTATAATGGATGGCAATGCTGGTCACTTAACTTTGT	122
Db	120	CATGGCGCTGCTCATCGTGGCACCGGTGTCTGGGCACAGCGGTGTATGTCTGCCTTCGT	179
QY	123	GGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCTGA	182
Db	180	GGCGACATCGAGCCTCCGACCCAGAACAACTTCTTCGCTCAACCTGGCCATCTCCGA	239
QY	183	CTTCCCTCGTGGGTTGATTTTCATTTCTGTACATCCCTCAAGTGTG---TTTAACTG	239
Db	240	CTTCTCGTGGCGGCTTGTGATCCCACTGTATGTACCTTAAGCTGTACAGCGCGCTG	299
QY	240	GAAATTTGGAAATGGAATCTGCATGTTTGGCTCATTAAGTAACTATCTTTTGTGACCGC	299
Db	300	GACCTTTCGGCGGGCGCTCTGCAAGCTGTGGCTGTAGTGAACTACCTGCTGTGCACCTC	359
QY	300	AATGCTCAACAATATGTCCTCATTTAGCTAACATGCAATGCAAGTTCCTCAATGCTGT	359
Db	360	CTTGGCTTCAACATCGTGTCTATCAGCTACAGACGCGCTTCTGTGCGTACCCGAGCGGT	419
QY	360	GTCCTTATAGGGCTCAACACATCTGGCATCATGAAGATGTTGGCTCAATAGGTGGCTGTTG	419
Db	420	CTCATACGGGGCCAGAGGGGTGACACGGGGGGGAGTGGCGGAAATGTGCTGGATGTG	479
QY	420	GATACTGGCTTCTTGTGTAAATGGCCCGATGATCTGGCTTCAGAT-----TCTTGGAA	473
Db	480	GGTGTGGCTCTTCCTGCTGTACGAGAACCACTCTGAACTGGAGATACCTGTGCCGGGG	539
QY	474	GAAACGACGAAACAAAGAGACTGGAGGCTGGCTTGTATTACAGAGTGGATACCTGCAC	533
Db	540	CAGCTCCATCCCGAGGGGCGACCTGTCTATGCCAGATTTCTTACAACTGGATCTCTCAT	599
QY	534	CATTACAAATGCTCTTGAATTCCTGCTTCCTGTGCATCTCTGGCTTATTTCAATGTACA	593
Db	600	CACGGCTTCCACCCTGGAGATTCTTAAAGCCCTTCTCAGAGTCACTTTCTTAAACCTCAG	659
QY	594	GATTTACTCGAGGCTGTGGAAAGCGTAAAGGCTCTCAG	629
Db	660	CATCTACTGGAACATCCAGAGGGCGACCCGCTCCG	695

RESULT 13
US-09-891-053-21
; Sequence 21, Application US/0989105321
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraoku
; APPLICANT: Takimura, Tetsuo

```

APPLICANT: Nakamura, Takao
APPLICANT: Kobayashi, Masahiko
APPLICANT: Tanaka, Ken-ichi
APPLICANT: Hidaka, Yutake
APPLICANT: Ohta, Masataka
TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
FILE REFERENCE: 06501-083001
CURRENT APPLICATION NUMBER: US/09/891,053
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: PCT/JP99/07280
PRIOR FILING DATE: 1999-12-24
PRIOR APPLICATION NUMBER: PCT/JP98/05967
PRIOR FILING DATE: 1998-12-25
PRIOR APPLICATION NUMBER: JP 11/145661
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 2050
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (271)...(1629)
US-09-891-053-21

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Query Match	11.9%	Score 140.4	DB 4	Length 2050
Best Local Similarity	53.6%	Prod. No. 1.1e-34		
Matches 341, Conservative	0	Mismatches 286	Indels 9	Gaps 2

[illegible]

594 GATTACTGAGCCTGTGGAAGCGTAGGCTCTCAG 629

Db 930 CATCTACCTGAACATCCAGAGCGGACCCGCTCCG 965

RESULT 14
US-09-949-016-5059
Sequence 5059, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5059
LENGTH: 2665
TYPE: DNA
ORGANISM: Human
US-09-949-016-5059

Query Match 11.9%; Score 140.4; DB 4; Length 2665;
Best Local Similarity 53.6%; Pred. No. 1.3e-34;
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

QY 3 GTCCGAGCTTAAACAGTACGATCTTGGACACAGCTGCTCAGGTCCTCCCTGGCATTTT 62
DB 351 GCGCGGGGCGGGGCGGGGCGCGGCTTCTCGGAGCGCTGACCGCGGTGCGCGCGCT 410
QY 63 AATGCTTATTTGCTTCTTGTATATATGTAAGCAATGCTGTGATCTTACCTTTT 122
DB 411 CATGGGCTGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 470
QY 123 GGTGACAGAAACCTTACATGATGATATTTTCTTAAATTTGCTATTTCTGA 182
DB 471 GCGCAGCTGAGGCTTCCGACCGAGAACATTTCTTCTGCTCAACCTGCGCATCTCGA 530
QY 183 CTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 239
DB 531 CTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 590
QY 240 GAATTTGGAATGGAATGCTGATGCTTTGGCTCATCTGACTATCTTTTGACCGC 299
DB 591 GACCTTGGCGCGGGGCTGCAAGCTGTGGCTGTGAGTACTGCTGCTGCACTTC 650
QY 300 ATCTGCTACAAATATGCTCTCATTTAGTACGATGATCAGTCAAGTCTTCAATGCTGT 359
DB 651 CTTCGCTTCAACATGCTGCTCATGCTACGACCGCTTCTGCTGCTGCTGCTGCTGCTGCT 710
QY 360 GTCTTATAGGCTCAACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 419
DB 711 CTTCATCCGCGGCGGCGGCTGACACGCGGCGGCGGAGTGGAGATCTGCTGCTGCTGCT 770
QY 420 GATPACGCTTTCTTGTGTAATGCGCCGATGATCTGCTGCTGCTGCTGCTGCTGCTGCT 473
DB 771 GGTGCTGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 830
QY 474 GAACAGACGAACACAAAGAGCTGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 533
DB 831 CAGCTCCATCCCGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 890
QY 534 CATTAACATGCTTCTGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 593
DB 891 CAGGCTTCCACCTGAGAGTCTTTCAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 950
QY 594 GATTTACTGAGAGCTGTGAGAGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 629

Db 951 CATCTACCTGAACATCCAGAGCGGACCCGCTCCG 986

RESULT 15
US-08-985-090-1
Sequence 1, Application US/08985090
Patent No. 5885893
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,090
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jean M. Silverl
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MN1-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2689 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 291..1625
US-08-985-090-1

Query Match 11.9%; Score 140.4; DB 2; Length 2689;
Best Local Similarity 53.6%; Pred. No. 1.3e-34;
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

QY 3 GTCCGAGCTTAAACAGTACGATCTTGGACACAGCTGCTCAGGTCCTCCCTGGCATTTT 62
DB 350 GCGCGGGGCGGGGCGGGGCGCGGCTTCTCGGAGCGCTGACCGCGGTGCGCGCGCT 409
QY 63 AATGCTTATTTGCTTCTTGTATATATGTAAGCAATGCTGTGATCTTACCTTTT 122
DB 410 CATGGGCTGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 469
QY 123 GGTGACAGAAACCTTACATGATGATATTTTCTTAAATTTGCTATTTCTGA 182
DB 470 GCGCAGCTGAGGCTTCCGACCGAGAACATTTCTTCTGCTCAACCTGCGCATCTCGA 529
QY 474 GAACAGACGAACACAAAGAGCTGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 533
DB 831 CAGCTCCATCCCGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 890
QY 534 CATTAACATGCTTCTGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 593
DB 891 CAGGCTTCCACCTGAGAGTCTTTCAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 950
QY 594 GATTTACTGAGAGCTGTGAGAGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 649

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QY 300 ATCTGCTACAAATATGTCCTCATTAAGTACGATCGATACAGTCAAGTTCAATGCTGT 359
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 650 CTCTGCTTCACATCATGCTGCTACAGTACGACCGCTTCTGTGCGTCAACCGAGCGGT 709
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 360 GTCTTAATAGGCTCAACACACTGSCATCATGAAGATTGTGCTCAATGCTGCTTTG 419
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 710 CTCATACCGGCGCCAGCAGGAGTACACGCGCGCGGCAGTGCGAAGATGCTGCTGTGTG 769
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 420 GATACCTGCTTTCTTGTAAATGCGCGATGATTCTGCGTTCAAGT-----TCTTGAA 473
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 770 GGTGCTGGCTTCTCTGCTGTACGACACGCAATCTGAGCTGGAGTACTGTTCGCGGG 829
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 474 GAACAGCACGACACAAAGAGCTGTGAGCTGTGCTTTGTACAGAGGTATCATCTCAC 533
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 830 CAGCTCCATCCCGAGGCGCACTGCTATGCGAGTTCTTACAACTGTAATTCCTCAT 889
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 534 CATTAACAATGCTTTGGAAATTCCTGCTTCTGTCAATCTGTGCTTATTCAATGTACA 593
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 890 CACGGCTTCACCCCTGAGTTCCTTAAGCCCTTCTCAGCGTCACTTCTTTAACTCAG 949
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 594 GATTACTGGAGCTGTGAAAGGCTAGGCTCTCAG 629
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 950 CATCTACCTGAACATCAGAGGCGCACCCGCTCCG 985
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Job time : 239 secs

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